

FIGURE 1

ACTGCACCTCGGTTCTATCGATTGAATTCCTCGGGGATCCTCTAGAGATCCCTCGACCTCGA
CCCACGCGTCCGGGCCGGAGCAGCACGGCCGAGGACCTGGAGCTCCGGCTCGCTCTTCCC
CAGCGCTACCCGCCATGCCGCTGCCGCGCGGGCCGCGCTGGGGCTCCTGCCGCTTCTGCTG
CTGTGCCGCCCCGCGCGGAGGCCGCCAAGAAGCCGACGCCCTGCCACCGGTGCCGGGGCT
GGTGACAAGTTTAAACAGGGGATGGTGACACCGCAAAGAAGAACTTTGGCGGCGGAACA
CGGCTTGGGAGGAAAAGACGTGTCCAAGTACGAGTCCAGCGAGATTCGCCTGCTGGAGATC
CTGGAGGGGCTGTGCAGAGCAGCGACTTCGAATGCAATCAGATGCTAGAGGCGCAGGAGGA
GCACCTGGAGGCTGGTGGCTGCAGCTGAAGAGCGAATATCCTGACTTATTTCGAGTGGTTTT
GTGTGAAGACACTGAAAGTGTGCTGCTCTCCAGGAACCTACGGTCCCAGCTGTCTCGCATGC
CAGGGCGGATCCAGAGGCCCTGCAGCGGAATGGCCACTGCAGCGGAGATGGGAGCAGACA
GGGCGACGGGTCTGCCGGTGCCACATGGGGTACCAGGGCCCGCTGTGCACTGACTGCATGG
ACGGCTACTTCAGCTCGCTCCGGAACGAGACCCACAGCATCTGCACAGCCTGTGACGAGTCC
TGCAAGACGTGCTCGGGCCTGACCAACAGAGACTGCGGCGAGTGTGAAGTGGGTGGGTGCT
GGACGAGGGCGCTGTGTGGATGTGGACGAGTGTGCGGCCGAGCCGCTCCCTGCAGCGCTG
CGCAGTTCTGTAAGAAGCCAAACGGCTCCTACAGTGCAGAGAGTGTGACTCCAGCTGTGTG
GGCTGCACAGGGGAAGGCCAGGAACTGTAAAGAGTGTATCTCTGGCTACGCGAGGGAGCA
CGGACAGTGTGCAGATGTGGACGAGTGTCTACTAGCAGAAAAAACCTGTGTGAGGAAAAACG
AAAACCTGCTACAATACTCCAGGGAGCTACGTCTGTGTGTCTCTGACGGCTTCGAAGAAACG
GAAGATGCCTGTGTGCCCGCGCAGAGGCTGAAGCCACAGAAGGAGAAAGCCGACACAGCT
GCCCTCCC CGAAGACCTGTAATGTGCCGACTTACCCTTTAAATATTCAGAAGGATGTCC
CGTGGAAAAATGTGGCCCTGAGGATGCCGTCTCCTGCAGTGGACAGCGCGGGGAGAGGCTGC
CTGCTCTCTAACGGTTGATTCTCATTTGTCCCTTAAACAGCTGCATTTCTTGGTTGTTCTTA
AACAGACTTGTATATTTTGATACAGTTCCTTTGTAATAAAATTGACCATTGTAGGTAAATCAGG
AGGAAAAAAAAAAAAAAAAAAAAAAAAAGGGCGGCCGCACTCTAGAGTCGACCTGCAGAAGC
TTGGCCGCCATGGCCCAACTTGTATTATGACGCTTATAATGGTTACAAATAAAGCAATAGCA
TCACAAATTTACAAATAAAGCAATTTTCTCACTGCATTCAGTTGTGGTTTGTCCAACTC
ATCAATGTATCTTATCATGTCTGGATCGGAATTAATTCGGCGCAGCACCATGGCCCTGAAAT
AACCTCTGAAAGAGGAACTGGTTAGGTACCTTCTGAGGCGGAAAGAACCCAGCTGTGGAATG
TGTGTCAAGTTAGGGTGTGGAAGTCCCAGGCTCCCAGCAGGCAGAAGTATGCAAGCATGC
ATCTCAATTAGTCAGCAACCCAGTTTT

FIGURE 2

><subunit 1 of 1, 353 aa, 0 stop
><MW: 38192, pI: 4.53, NX(S/T): 2
MRLPRRAALGLLPLLLLLPPAPEAAKKPTPCHRCRGLVDKFNQGMVDTAKKNFPGGGNTAWEEKTL SKYESSEIRL
LEILEGLCESSDFECNQMLEAQEEHLEAWWLQLKSEYDPLFEWFCVKTLKVVCCSPGT YGPDCLACQGGSQRPCSG
NGHCSGDGSRQGDGSCRCHMGYQGGLCTDCMDGYFSSLRNETHS ICTACDESKCTCSGLTNRDCGECEVGWVLDE
GACVDVDECAAEPPPCSAAQFCKNANGSYTCCEEDSSCVGCTGEGPGNCKECISGYAREHGQCADVDECSLA EKT
CVRXNENCYNTPGSYVVCVCPDGEETEDACVPPAEAEATEGESPTQLPSREDL

Signal peptide:

amino acids 1-24

N-glycosylation sites.

amino acids 190-194 and 251-255

Glycosaminoglycan attachment sites.

amino acids 149-153 and 155-159

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 26-30

Casein kinase II phosphorylation sites.

amino acids 58-62, 66-70, 86-90, 197-201, 210-214, 255-259, 295-299, 339-343
and 349-353

Tyrosine kinase phosphorylation site.

amino acids 303-310

N-myristoylation sites.

amino acids 44-50, 54-60, 55-61, 81-87, 150-156, 158-164, 164-170, 252-258 and
313-319

Aspartic acid and asparagine hydroxylation site.

amino acids 308-320

EGF-like domain cysteine pattern signature.

amino acids 166-178

Leucine zipper pattern.

amino acids 94-116

FIGURE 3

CAGGTCCAACCTGCACCTCGGTTCTATCGATTGAATTCCTCCGGGGATCCTCTAGAGATCCCTC
GACCTCGACCCACGCGTCCGCCAGGCCGGGAGGCGACGCGCCAGCCGCTCTAAACGGGAACA
GCCCTGGCTGAGGGAGCTGCAGCGCAGCAGAGTATCTGACGGCGCCAGGTTGCGTAGGTGCG
GCACGAGGAGTTTTCCCGGCAGCGAGGAGGTCTTGAGCAGC**ATGG**CCCGGAGGAGCGCCTTC
CCTGCCGCCGCGCTCTGGCTCTGGAGCATCCTCCTGTGCCTGCTGGCACTGCGGGCGGAGGC
CGGGCCGCCGAGGAGGAGACCTGTACCTATGGATCGATGCTCACCAGGCCAAGAGTACTCA
TAGGATTTGAAGAAGATATCCTGATTGTTTTCAGAGGGGAAAATGGCACCCTTTACACATGAT
TTCAGAAAAGCGCAACAGAGAATGCCAGCTATTCTGTCAATATCCATTCCATGAATTTTAC
CTGGCAAGCTGCAGGGCAGGCAGAAATACTTCTATGAATTCCTGTCTTGGCTCCCTGGATA
AAGGCATCATGGCAGATCCAACCGTCAATGTCCCTCTGCTGGGAACAGTGCCTCACAAGGCA
TCAGTTGTTCAAGTTGGTTTCCCATGTCTTGGAAGAACAGGATGGGGTGCCAGCATTGGAAGT
GGATGTGATTGTTATGAATCTGAAGGCAACACCATTCTCCAAACACCTCAAATGCTATCT
TCTTTAAACATGTCAACAAGCTGAGTGCCAGGCGGGTGCCGAAATGGAGGCTTTTGTAAAT
GAAAGACGCATCTGCGAGTGTCTGTATGGGTTCCACGGACCTCCTGTGAGAAAGCCCTTGG
TACCCACAGATGTATGAATGGTGGACTTGTGTGACTCCTGGTTTCTGCATCTGCCCACTCG
GATTCTATGGAGTGAACCTGTGACAAAGCAAACTGCTCAACCACCTGCTTTAATGGAGGGACC
TGTTTCTACCTGGAATAATGATTGTCCTCCAGGACTAGAGGGAGAGCAGTGTGAATCAG
CAATATGCCACAACCTGTGCAAAATGGAGGTAAATGCATTGGTAAAAGCAAAATGTAAGTGTT
CCAAAGGTTACCAAGGAGACCTCTGTTCAAAGCCTGTCTGCGAGCCTGGCTGTGGTGACAT
GGAACCTGCCATGAACCCAACAATGCCAATGTCAAGAAGGTTGGCATGGAAGACACTGCAA
TAAAGGTACGAAGCCAGCCTCATACATGCCCTGAGGCCAGCAGGCGCCAGCTCAGGCAGC
ACACGCCTTCACTTAAAAAGGCCGAGGAGCGCGGGATCCACCTGAATCCAATTACATCTGG
TGAACTCCGACATCTGAAACGTTTAAAGTTACACCAAGTTATAGCCTTTGTTAACTTTCA
TGTGTTGAATGTTCAAATAATGTTCAATTACACTTAAGAATACTGGCCTGAATTTTATTAGCT
TCATTATAAATCACTGAGCTGATATTTACTCTTCTCTTTTAAAGTTTCTTAAGTACGCTCTAG
CATGATGGTATAGATTTTCTGTGTTTCACTGCTTTGGGACAGATTTTATATTATGTCAATTGA
TCAGGTTAAAAATTTTCACTGTGTAGTTGGCAGATATTTTCAAATTACAATGCATTATGGT
GTCTGGGGGCAGGGGAACATCAGAAAGGTTAAATGGGCAAAATGCGTAAGTACAAGAAT
TTGGATTGGTCAGTTAATGTTGAAGTTACAGCATTTCAGATTTTATTGTGAGATATTTAGAT
GTTTGTGTACATTTTAAAAATGTCTTAAATTTTAAACTCTCAATACAATATATTTTGACC
TTACCATATTTCCAGAGATTCACTATTAATAAAAAAAAAAATTAACATGTGGTAGTGGCATT
AAACAATATAATATATTCTAAACACAATGAAATAGGGAATATAATGTATGAATTTTGTGAT
TGGCTTGAAGCAATATAATATATTGTAAACAAAACACAGCTCTTACCTAATAAACATTTTAT
ACTGTTTGTATGTATAAAATAAAGGTGCTGCTTTAGTTTTTTGGAAAAAATAAAAAAAAAA
AAAAAAAAAAAAAAAAAAAAAAAAAGGGCGCGCATCTAGAGTCGACCTGCAGAAGCTTGGC
CGCCATGGCCCACTTGTATTATGCAGCTTATAATG

FIGURE 4

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></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA33094
><subunit 1 of 1, 379 aa, 0 stop
><MW: 41528, pI: 7.97, NX(S/T): 2
MARRSAFPAALWLWSILLCLLALRAEAGPPQEESLYLWIDAHQARVLIGFEEDILIVSEGK
MAPFTTHDFRKAQQRMFAIPVNIHSMNFTWQAAGQAEYFYEFLLSLRSLDKGIMADPTVNVPLL
GTVPHKASVVQVGFPCLGKQDGVAAFEVDVIVMNSEGNITLQTPQNAIFFKTCQQABCPGGC
RNGGFCNERRICECPDGFHGFHCEKALCTPRCMNGGLCVTPGFCICPPGFYGVNCDKANCST
TCFNGGTCFYPGKCICPPGLEGEQCEISKCPQPCRNGGKIGKSKCKCSKGYQGDLCSKPVK
EPGCGAHGTCHEPNKCQCQEGWHGRHCNKRYEASLIHALRPAGAQLRQHTPSLKKAERDRP
PESNYIW
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Signal peptide:

amino acids 1-28

N-glycosylation site.

amino acids 88-92, 245-249

Casein kinase II phosphorylation site.

amino acids 319-323

Tyrosine kinase phosphorylation site.

amino acids 370-378

N-myristoylation sites.

amino acids 184-190, 185-191, 189-195, 315-321

ATP/GTP-binding site motif A (P-loop).

amino acids 285-293

EGF-like domain cysteine pattern signature.

amino acids 198-210, 230-242, 262-274, 294-306, 326-338

FIGURE 5

CGGACGCGTGGGCGTCCGGCGGTGCGAGAGCCAGGAGGCGGAGGCGCGGGGCCAGCCTGGG
CCCCAGCCCACACCTTCACCAGGGCCAGGAGGCCACCAATGTGGGCGATGTCCACTGGGGCTAC
TGCTGTTGCTGCCGCTGGCTGGCCACTTGGCTCTGGGTGCCAGCAGGGTTCGTGGGCGCGG
GAGCTAGCACCGGCTCTGCACCTGCGGGGCATCCGGGACGCGGGAGGCGCGTACTGCCAGGA
GCAGGACCTGTGCTGCCGCGGCGGTGCCGACGACTGTGCCCTGCCCTACCTGGGCGCCATCT
GTTACTGTGACCTCTTCTGCAACCGCACGGTCTCCGACTGCTGCCCTGACTTCTGGGACTTC
TGCCCTCGGCGTGCCACCCCTTTTCCCCCGATCCAAGGATGTATGCATGGAGGTCTATCTA
TCCAGTCTTGGGAACGTACTGGGACAACTGTAAACGTTGCACCTGCCAGGGAACAGGCAGT
GGCATGTGTGGATCCAGACATGATCAAAGCCATCAACCAGGGCAACTATGGCTGGCAGGCTGG
GAACCACAGCGCCTTCTGGGGCATGACCTGGATGAAGGGCATTGCTACCGCTGGGCACCA
TCCGCCCATCTTCTCGGTATGAACATGCATGAAATTTATACAGTGCTGAACCCAGGGGAG
GTGCTTCCACAGCCCTTCGAGGCTCTGAGAAGTGGCCAACTGATTCATGAGCCTCTTGA
CCAAGGCAACTGTGCAGGCTCTGGGCCTTCTCCACAGCAGCTGTGGCATCCGATCGTGTCT
CAATCCATTCTCTGGGACACATGACGCTGTCTGTGCGCCCAAGACCTGCTGTCTTGTGAC
ACCCACAGCAGCAGGGCTGCCGCGGTGGGCGTCTCGATGGTGCCTGGTGGTTCTGCGCTCG
CCGAGGGGTGGTGTCTGACCACTGCTACCCCTTCTCGGGCCGTGAACGAGACGAGGCTGGCC
CTGCGCCCCCTGTATGATGCACAGCCGAGCCATGGGTGGGGCAAGCGCCAGGCCACTGCC
CACTGCCCCAACAGCTATGTTAATAACAATGACATCTACCAGGTCACTCCTGTCTACCGCCT
CGGCTCCAACGACAAGGAGATCATGAAGGAGCTGATGGAGAATGGCCCTGTCCAAGCCCTCA
TGGAGGTGCATGAGGACTTCTTCTATACAAGGGAGGCATCTACAGCCACACGCCAGTGAGC
CTTGGGAGGCCAGAGAGATACCGCCGGCATGGGACCACTCAGTCAAGATCACAGGATGGGG
AGAGGAGACGCTGCCAGATGGAAGGACGCTCAAATACTGGACTGCGGCCAATCCTGGGGCC
CAGCCTGGGGCGAGAGGGGCCACTTCCGCATCGTGCCGGCGTCAATGAGTGCACATCGAG
AGCTTCGTGCTGGGCGTCTGGGGCCGCTGGGCATGGAGGACATGGGTCACTAGGCGTG
CGGGCACACGCGGGGTCCGGCTGGGATCCAGGCTAAGGGCCGGCGGAAGAGGCCCAATG
GGGCGGTGACCCAGCCTCGCCGACAGAGCCCGGGGCGCAGGGGGCGCCAGGGCGCTAAT
CCGGGCGCGGGTTCCGCTGACGCAGCGCCCCGCTGGGAGCCGCGGCGAGGCGAGACTGGCG
GAGCCCCAGACCTCCAGTGGGGACGGGGCAGGGCCTGGCCTGGGAAGAGCACAGCTGCGAG
ATCCAGGCCTCTGGGCCCCCACTCAAGACTACCAAAGCCAGGACACCTCAAGTCTCCAGC
CCCAATACCCACCCCAATCCCGTATTCTTTTTTTTTTTTTTTTGTAGACAGGGTCTTGCTCCG
TTGCCAGGTTGGAGTGCAGTGGCCATCAGGGCTCACTGTAAACCTCCGACTCCTGGGTTC
AGTGACCTCCCACTCAGCCTCTCAAGTAGCTGGGACTACAGGTGCAACCACACACCTGGC
TAATTTTTGTATTTTGTAAAGAGGGGGGTCTCACTGTGTTGCCAGGCTGGTTTCGA
CTCTGGGCTCAAGCGTTCCACTGCCTCCGCTCCCAAAGTGCTGGGATTGCAGGCATGAGCC
ACTGCACCCAGCCCTGTATCTTATTCTTCAGATATTTATTTTCTTTTCACTGTTTAAAA
TAAACCAAAGTATTGATAAAAAAAA

FIGURE 6

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA33223
><subunit 1 of 1, 164 aa, 1 stop
><MW: 18359, pI: 7.45, NX(S/T): 1
MWRCPLGLLLLLPLAGHLALGAQQGRGRRELAPGLHLRGIRDAGGRYCQEQLCCRGRADDC
ALPYLGAICYCDLFCNRTVSDCCPDFWDFCLGVPPPPFPIQGCMHGGRIYPVLGTYWDNCNR
CTCQENRQWHGGSRHDQSHQPGQLWLAGWEPQRLLGHDPG

N-glycosylation site.

amino acids 78-82, 161-165

Casein kinase II phosphorylation site.

amino acids 80-84, 117-121, 126-130, 169-173, 205-209, 296-300,
411-415

N-myristoylation site.

amino acids 21-27, 39-45, 44-50, 104-110, 160-164, 224-230,
269-275, 378-384, 442-448

Amidation site.

amino acids 26-30, 318-322

Eukaryotic thiol (cysteine) proteases histidine active site.

amino acids 398-409

FIGURE 7

AGGCTCCTTGGCCCTTTTCCACAGCAAGCTTNTGCNATCCCGATTTCGTTGTCTCAAATCCA
ATTCTCTTGGGACACATNACGCCTGTCCTTTNGCCCCAGAACCTGCTGTCTTGTACACCCAC
CAGCAGCAGGGCTGCCGCGNTGGGCGTCTCGATGGTGCCCTGGTGGTTCCTGCGTCGCCGAGG
GNTGGTGTCTGACCACTGCTACCCCTTCTCGGGCCGTGAACGAGACGAGGCTGGCCCTGCGC
CCCCCTGTATGATGCACAGCCGAGCCATGGGTGCGGGCAAGCGCCAGGCCACTGCCCACTGC
CCCAACAGCTATGTTAATAACAATGACATCTACCAGGTCACTCCTGTCTACCGCCTCGGCTC
CAACGACAAGGAGATCATGAAGGAGCTGATGGAGAATGGCCCTGTCCAAGCCCTCATGGAGG
TGCATGAGGACTTCTTCCTATACAAGGGAGGCATCTACAGCCACACGCCAGTGAGCCTTGGG
AGGCCAGAGAGATACGCCCGCATGGGACCCACTCAG

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FIGURE 8

GCTGCTTGCCCTGTTGATGGCAGGCTTGGCCCTGCAGCCAGGCACTGCCCTGCTGTGCTACT
CCTGCAAAGCCCAGGTGAGCAACGAGGACTGCCTGCAGGTGGAGAACTGCACCCAGCTGGGG
GAGCAGTGCTGGACCGCGCATCCGCGCAGTTGGCCTCCTGACCGTCATCAGCAAAGGCTG
CAGCTTGAATGCGTGGATGACTCACAGGACTACTACGTGGGCAAGAAGAACATCACGTGCT
GTGACACCGACTTGTGCAACGCCAGCGGGGCCCATGCCCTGCAGCCGGCTGCCGCCATCCTT
GCGCTGCTCCCTGCACTCGGCCTGCTGCTCTGGGGACCCGGCCAGCTATAGGCTCTGGGGGG
CCCCGCTGCAGCCCACACTGGGTGTGGTGCCCCAGGCCTCTGTGCCACTCCTCACAGACCTG
GCCCAGTGGGAGCCTGTCTGTTCTCTGAGGCACATCCTAACGCAAGTCTGACCATGTATGT
CTGCACCCCTGTCCCCACCCCTGACCCCTCCCATGGCCCTCTCCAGGACTCCCACCCGGCAGA
TCAGCTCTAGTGACACAGATCCGCCTGCAGATGGCCCTCCAACCCTCTCTGCTGCTGTTTC
CATGGCCCAGCATTCTCCACCCTTAACCCTGTGCTCAGGCACCTCTTCCCCCAGGAAGCCTT
CCCTGCCCCACCCCATCTATGACTTGAGCCAGGTCTGGTCCGTGGTGTCCTCCGCACCCAGCA
GGGGACAGGCACTCAGGAGGGCCAGTAAAGGCTGAGATGAAGTGGACTGAGTAGAACTGGA
GGACAAGAGTCGACGTGAGTTCTCTGGGAGTCTCCAGAGATGGGGCCTGGAGGCCTGGAGGAA
GGGGCCAGGCCTCACATTGCTGGGGCTCCCTGAATGGCAGCCTGAGCACAGCGTAGGCCCTT
AATAAACACCTGTTGGATAAGCCAAAAAAA

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FIGURE 9

MTHRTTTWARRTSRAVTPTCATPAGPMPCSRLPFSLRCSLHSACCSGDPASYRLWGAPLQPT
LGVVVPQASVPLLTDLAQWEPVLVPEAHPNASLTMVYCTPVPHPDFPMALSRTPTRQISSSDT
DPPADGPSNPLCCCFHGPAFSTLNFVLRHLFPQEAFPAHPIYDLSQVWSVVSPAPSRGQALRRAQ

Signal peptide:

amino acids 1-47

N-glycosylation site.

amino acids 31-35, 74-78, 84-88

Casein kinase II phosphorylation site.

amino acids 22-26, 76-80

N-myristoylation site.

amino acids 56-60

Amidation site.

amino acids 70-74

Abstract The purpose of this study was to determine the effect of a 12-week, low-intensity, supervised walking program on the physical and psychological health of sedentary, middle-aged women. The study was a randomized, controlled trial. The subjects were 40 sedentary, middle-aged women who were randomly assigned to either a supervised walking program or a control group. The walking program consisted of 12 weeks of supervised walking, 3 times per week, for 30 minutes per session. The control group consisted of 20 women who did not participate in the walking program. The subjects were assessed at baseline and at 12 weeks. The walking program had a significant positive effect on the physical and psychological health of the subjects. The walking program significantly improved the subjects' physical health, as measured by the 6-minute walk test, and their psychological health, as measured by the Beck Depression Inventory and the State-Trait Anxiety Inventory. The walking program also had a significant positive effect on the subjects' quality of life, as measured by the SF-36. The walking program was well tolerated and had no adverse effects. The results of this study suggest that a supervised walking program can be an effective intervention for improving the physical and psychological health of sedentary, middle-aged women.

CCACGCGTCCGAACCTCTCCAGCGATGGGAGCCGCCCGCTGTGTGCCAACCTCACTCTGT
GCTTACAGCTGCTGATTCTCTGCTGTCAAACCTCAGTACGTGAGGGACCAGGGCGCCATGACC
GACCAGCTGAGCAGGCGGCAGATCCGCGAGTACCAACTCTACAGCAGGACCAGTGGCAAGCA
CGTGACAGTTCACCGGGCGTTCGCATCTCCGCCACCGCCGAGGACGGCAACAAGTTTGCCAAG
TCATAGTGGAGACGGACACGTTTGGCAGCCGGGTTCGCATCAAAGGGGCTGAGAGTGAGAAG
TACATCTGTATGAACAAGAGGGGCAAGCTTCATCGGGAAGCCAGCGGGAAGAGCAAAAGACTG
CGTGTTACCGGAGATCGTGCTGGAGAAACACTATACGGCCTTCCAGAACGCCCGGCACAGAGG
GCTGTTCTATGGCCTTACCGCGGACGGGCGCGCCCGCCAGGCTTCCCGCAGCCGCCAGAAC
CAGGCGGAGGCCCACTTCATCAAGCCGCTTACCAAGGCCAGTGCCTTCCCCAACCCACGC
CGAGAAGCAGAAGCAGTTCGAGTTTGTGGGCTCCGCCCCACCCGCGGACCAAGCGCACAC
GGCGGCCCCAGCCCCCTACGCTAGCTCTGGGAGGCAGGGGGGCAGCAGCCCCGTGGGCGCCTCCC
CACCCCTTTCCCTTCTTAATCCAAGGACTGGGCTGGGGTGGCGGGAGGGGAGCCAGATCCCC
GAGGGAGGACCCTGAGGGCCGCGAAGCATCCGAGCCCCCAGCTGGGAAGGGGCAGGCCCGTG
CCCCAGGGGCGGCTGGCACAGTGGCCCCCTTCCCGGACGGGTGGCAGGCCCTGGAGAGGAAT
GAGTGTCAACCCTGATCTCAGGCCACCAAGCCTCTGCCGGCTCCCAGCCGGGCTCCTGAAGCC
CGCTGAAAGGTACAGCGACTGAAGGCCTTGACAGACAACCGTCTGGAGGTGGCTGTCTCTCAAAA
TCTGCTTCTCGGATCTCCCTCAGTCTGCCCCAGCCCCCAAACCTCTCTGGCTAGACTGTA
GGAAGGGACTTTTGTTTGTGTTTGTTCAGGAAAAAGAAAGGGAGAGAGAGGAAAAATAG
AGGGTGTCCCACTCTTCACATTCACGACCCAGGCCCTGCACCCCCCACTCCAGGCC
CGGAATAAAACCACTTCTGTC

FIGURE 11

MGAARLLPNLTLCQLLILCCQTQYVRDQGAMTDQLSRRQIREYQLYSRTSGKHVQVTGRRISATAEDGNKFAKLIVETDTFGSRVRIKGAESEKYICMNRGKLGKPSGKSKDCVFTEIVLENNYTAFQNAHEGWFMATFRQGRPRQASRSRQNRQEAHFIRKRLYQGQLPFPNHAEKQKQFEFVGSAPTRRTKRTRRPQPLT

Signal peptide:

amino acids 1-22

N-glycosylation site.

amino acids 9-13, 126-130

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 60-64

Casein kinase II phosphorylation site.

amino acids 65-69

Tyrosine kinase phosphorylation site.

amino acids 39-48, 89-97

N-myristoylation site.

amino acids 69-75, 188-194

Amidation site.

amino acids 58-62

HBGF/FGF family signature.

amino acids 103-128

FIGURE 12

ACTTGCCATCACCTGTTGCCAGTGTGGAAAAATTCCTCCTGTTGAATTTTTTGCACATGGAG
GACAGCAGCAAAGAGGGGCAACACAGGCTGATAAGACCAGAGACAGCAGGGGAGATTATTTTAC
CATACGCCCTCAGGACGTTCCCTCTAGCTGGAGTTCTGGACTTCAACAGAACCCCATCCAGT
CATTTTGAATTTGCTGTTTATTTTTTTTTTCTTTTCTTTTCCCACCACATTGTATTTTAT
TTCCGTACTTTCAGAAATGGGCGCTACAGACCACAAAGTGGGCCAGCCATGGGGCTTTTTTCCT
GAAGCTTTGGCTTATCATTTCCCTGGGGCTCTACTCACAGGTGTCCAAATCCTTGGCCTTGC
CTAGTGTGTGCCGTGCGACAGGAACCTTGTCTACTGTAAGACGAGCTTGACCTCAGTG
CCTCTTGGGATCCCGGAGGGCGTAACCGTACTCTACCTCCACAACCAAATTAATAATGTC
TGGATTTCTGTCAGAACTGCACAATGTACAGTCGGTGCACAGGTCTACCTGTATGGCAACC
AACTGGACGAATTCCTCATGAACCTTCCCAGAAATGTCAGAGTTCTCCATTGTCAGGAAAAAC
AATATTACAGCCATTTACGGGCTGCTCTTGGCCAGCTCTTGAAGCTTGAAGAGCTGCACCT
GGATGACAACCTCCATATCCACAGTGGGGGTGGAAGACGGGGCTTCCGGGAGGCTATTAGCC
TCAAATTGTTGTTTTGTCTAAGAATCACCTGAGCAGTGTGCCTGTTGGGCTTCTGTGGAC
TTGCAAGAGCTGAGAGTGGATGAAAAATCGAATTGCTGTCTATATCCGACATGGCCTTCCAGAA
TCTCACAGCTTGGAGCGTCTTATTGTGGACGGGAACCTCCTGACCAACAAGGGTATCGCCG
AGGCACGCTTCAGGAAGCTCACCAAGCTCAAGGAATTTTCAATTGTACGTTATTCGCTGTCC
CACCTCCTCCCGATCTCCAGGTACGCATCTGATCAGGCTCTATTGTGAGGACAACCAGAT
AAACCACATTCCTTTGACAGCCTTCTCAAATCTGCGTAAGCTGGAACGGCTGGATATATCCA
ACAACCAACTGCGGATGCTGACTCAAGGGGTTTTTGATAATCTCTCCAACTGAAGCAGCTC
ACTGCTCGGAATAACCTTGGTTTTGTGACTGCAGTATTAATGGGTACAGAAATGGCTCAA
ATATATCCCTTATCTCTCAACGTGCGGGGTTTCATGTGCCAAGGTCTGAAACAAGTCGGG
GGATGGCGCTCAGGGAATTAATATGAATCTTTGTCTGTCCACACAGCAGCCCGGGCTG
CCTCTCTTACCCCCAGCCCCAAGTACAGCTTCTCCGACCACTCAGCCTCCCAACCTCTCTAT
TCCAAACCTTAGCAGAAGCTACACGCCTCCAACCTCTACCACATCGAAACTTCCACGATTC
CTGACTGGGATGGCAGAGAAAGAGTGACCCACCTATTTCTGAACGGATCCAGCTCTCTATC
CATTTTGTGAATGATACTTCCATTCAAGTCAGCTGGCTCTCTCTTTCACCGTGATGGCATA
CAAACCTCACATGGGTGAAAAATGGGCCACAGTTTAGTAGGGGGCATCGTTCAGGAGCGCATAG
TCAGCGGTGAGAAGCAACACCTGAGCCTGGTTAACTTAGAGCCCCGATCCACCTATCGGATT
TGTTTAGTGCCACTGGATGCTTTTAACTACCGCGCGGTAGAAGACACCAATTTGTTTCAGAGGC
CACCACCCATGCCTCTATCTGAACAACGGCAGCAACACAGCGTCCAGCCATGAGCAGACGA
CGTCCCACAGCATGGGCTCCCCCTTTCTGCTGGCGGGCTTGATCGGGGGCGCGGTGATATTT
GTGCTGGTGGTCTTGTGACGCTCTTTGTGCTGGCATATGCAAAAAAGGGGCGCTACACCTC
CCAGAAGTGGAATAACAACGGGGCGCGCGGAAAGATGATTATTGCGAGGCGGCACCAAGA
AGGACAACCTCCATCTGGAGATGACAGAAACCAAGTTTTCAGATCGTCTCTTAAATAACGAT
CAACTCTTAAAGAGAGATTTTCAGACTGCAAGCCATTTACACCCCAATGGGGGCATTAATTA
CAGACACTGCCATATCCCCAACACATCTGCGATACTGCAACAGCAGCGTGCAGACCTGGAGC
ACTGCCATACGTGACAGCAGAGGCCAGCGTTATCAAGCGGACCAATTAGACTCTTGAGAC
CACACTCGTGTGTGACATAAAGACACGCAGATTAATTTGATAAATGTTACACAGATGCAT
TTGTGCATTTGAATACTCTGTAATTTATACGGGTGACTATATATATGGGATTAAAAAAGTG
CTATCTTTTCTATTTCAGTATAATTACAAACAGTTTTGTAACTCTTTGCTTTTAAATCTT

FIGURE 13

MGLQTTKWPSHGAFFLKSWLIISLGLYSQVSKLLACPSVCRCDRNFVYCNERSLTSVPLGIP
EGVTVLYLHNNQINNAGFPAELHNVQSVHTVYLYGNQLDEFPMNLPKNVRVLHLQENNIQTI
SRAALAQLLKLELHLLDDNSISTVGVEDGAFREAI SLKLLFLSKNHLSSVPVGLPVDLQELR
VDENRIAVISDMAFQNLTSLERLIVDGNLLTNKGIAEGTFSHLTKLKEFSIVRNSLSHPPPD
LPGTHLIRLYLQDNQINHIPLTAFSNLRKLERLDISNNQLRMLTQGVFDNLSNLKQLTARNN
PWFCDCSIKWVTEWLKYIPSSLNVRGFMCGQPEQVRGMAVRELNMNLLSCPTTTPGLPLFTF
APSTASPTQPPTLSIPNPSRSYTPPTPTTSKLPTIPDWDGRERVTPPISERIQLSIHFVND
TSIQVSWLSLFTVMAYKLTWVKMGHSLVGGIVQERIVSGEKQHLSLVNLEPRSTYRICLVPL
DAFNRYRAVEDTICSEATTHASYLNNGSNTASSHEQTTSMSMGSPFLLAGLIGGAVIFVLVVL
LSVFCWHMHKKGRYTSQKWYKNGRRKDDYCEAGTKKDNSILEMTETSFIQIVSLNNDQLLKG
DFRLQPIYTPNGGINYTDCHIPNNMRYCNSSVPDLEHCHT

Signal peptide:

amino acids 1-42

Transmembrane domain:

amino acids 542-561

N-glycosylation site.

amino acids 202-206, 298-302, 433-437, 521-525, 635-639, 649-653

Casein kinase II phosphorylation site.

amino acids 204-208, 407-411, 527-531, 593-597, 598-602, 651-655

Tyrosine kinase phosphorylation site.

amino acids 319-328

N-myristoylation site.

amino acids 2-8, 60-66, 149-155, 213-219, 220-226, 294-300,
522-528, 545-551, 633-639

Amidation site.

amino acids 581-585

Leucine zipper pattern.

amino acids 164-186

Phospholipase A2 aspartic acid active site.

amino acids 39-50

FIGURE 14

ACTTGGAGCAAGCGGCGCGGAGACAGAGGCAGAGGCAGAAGCTGGGCTCCGCTCTCGCCTCCCACGAGCG
ATCCCGAGGAGAGCGCGGCCCTTCGGCGAGGCGAAGAGGCCGAGGAAAGACCCGGGTGGCTGGCGCCCTGGC
TCGCTTCCAGGCGCGCGGCGCTGCAGCCTTGGCCCTCTTGCTCGCCTTGAAATGTAAGAAAGATGTCTCGAGGCT
GCTTTCCTGCTATCTCTCGACAGATCTGCTCTCTCTCTCGGAGGCTGCTCAATATGGCAGCAGCTGTCAAGAAATG
CTAGGGGACAGACGCTCGGACCCACCCCGACAGCGGCCCTTCTGGAGAGTTCTCTGAGAAACAGCGGGGACAGCC
TGCTTTTTCATCATTTGACAGCTCTCGCAGTGTCAACACCCATGACTATGCAAAAGGTCAAGGAGTTTCATCGTGGACA
TCTTGCAATTCTTGACATTTGGTCTGTGATGTCAACCCGAGTGGGCTGCTCAATATGGCAGCAGCTGTCAAGAAATG
AGTTTCTCCTCAAGACCTTCAAGAGGAAGTCCGAGGTTGGAGCGTGTCTCAAGAGGATGCGGCATCTGTCAACGG
GCACCATGACTGGGCTGGCCATCCAGTATGCCCCGAAACATCGCATTTCTGAAAGCAGAGGGGGGCCCGGCCCTGA
GGGAGAAATGTGCCACGGGTCAATAATGATCGTGACAGATGGGAGACCTCAGGACTCCGCTGGCCGAGGTGGCTGCTA
AGGACCGGACACGGGCATCTTAATCTTTGGCATTGGTGTGGCCAGGTAGACTTCAACACCTTGAAGTCAATG
GGAGTGAGCCCATGAGGACCATGCTTCTCTGTGGCCAAATTCAGCCAGATTGAGACGCTGACCTCCGTGTTC
AGAAGAAGTTGTGACAGGCCCATCATGTGACAGCACCCTGGAGCATAACTGTGCCCACTTCTGCATCAACATCCCTG
GCTCATACTGTGACAGGTGCAAAACAGGCTCATTTCTCAACTCGGATCAGACGACTTGCAGAAATCCAGGATCTGT
GTCCATGGAGGACCAACTGTGACAGCTCTGTGTAAATGTGCCGGGCTCCTTCGTCTGCCAGTGCTACAGTG
GTGACGCCCTGGCTGAGGATGGGAAGAGGTGTGTGGCTGTGGACTACTGTGCTCAGAAAACACCGGATGTGAAC
ATGAGTGTGTAATGTGATGGCTCTTACCTTTGCGAGTCCATGAAGGATTTGTCTTAAACCCTGAAGAAAA
CGTGACAAAGGATCAACTACTGTGCACTGAAACAAACCGGGCTGTGAGCATGAGTGCCTCAACATGGAGGAGAGCT
ACTACTGCCCTGCCACCGTGGCTACACTCTGGACCCCAATGGCAAAACCTGACGCCGAGTGGACCACTGTGCAAC
AGCAGGACCATGCTGTGAGCAGCTGTGTCTGAACACGAGGAGTTTCTTCGTCTGCCAGTGTCTCAGAAAGCTCTCC
TCATCAACGAGGACCTCAAGACCTGTCTCCGGGTGGATTACTGCCCTGTGAGTGACCATTCGTCTTAAACCCTGAAGAAAA
GTGTCAACATGGACAGATCCTTTGCCCTGTGAGTGTCTGAGGACACGCTGTCTCCGACGAGTGGGAAGAGCTGTG
CAAAATTTGGACTCTTGTGCTCTGGGGGACACGGTTGTGAACATTCGTGTGAAGCAGTGAAGATTCGTTCGTGT
GCCAGTGTCTTGAAGGTTATATGCTCCGTGAAGATGGAAGAACTTGCAGAGGAAAGATGTCTGCCAGCTATAG
ACCATGGCTGTGAACACATTTGTCTCCGTGAAGATGGAAGAACTTGCAGAGGAAAGATTCGCTTCG
CTGAGGATGGGAAGCTCGCCGAGGAAGAGATGTCTGCAAAATCAACCCACCATGGCTGCGAACACATTTGTGTTA
ATAATGGGAATTCCTACTCTGCAAAATGCTCAGAGGATTTGTCTAGCTGAGGACGAGAAAGCGGTGCAAGAAAT
GCACTGAAGGCCCAATTTGAGCTGGCTCTTTGTGATCGATGATCCAGAGTCTTGGAGAGAGAAATTTGAGGTG
TGAGCAGCTTTGTCTGCAATTAAGATTTCTTGCAAAATTTCCCAAGCGCTCCAGTGGGGCTGTCTCAGT
ATTCCACACAGGTCTCAACACAGATTTCACTCTGAGAACTTCAACTCAGCCAAAGACATGAAAAGAGCGCTGGCCC
ACATGAATATCATGGGAAGAGGCTCTATGACTGGCTGGCCCTGAAACAGATTTTGGAGAGAAATTTACCCAG
GAGAAGGGGCCAGGCCCTTTCCACAAAGGTTGCCAGAGCAGCCTATGTTTCCAGCGCGGACGGGCTCAGGATG
ACGTCTCGAGTGGGCAAGTAAAGCCAAAGCCAAATGTGTATCACTATGTATGCTGTTGGGGTAGGAAAAGCCATTG
AGGAGGAATCAAGAGATTTGCCCTCTGAGCCCAACAAACAGCAGCTCTCTATGCGCGAGACTTCAGCAATGG
ATGAGATAGTGAAGAACTCAAGAAAGGATCTGTGAAGCTCTAGAAGACTCCGATGGAAGACAGGACTCTCCAG
CAGGGGAACTGCCAAAACGCTTCAACAGGCCAAGAAATCTGAGCCAGTCAACCATAAATTTCAAGAGCTTCTT
CTGTCTTCAATTTTTCAGTGTCAACACAGATATCTGTTTGAAGAGCAATCTTTTACGCTCTACAACAAAGCTTT
CCCATTCACAAAACCTTCAGGAAGCCCTTTGGAAGAAAAACACGATCAATGTGAAGTGAAGAACTTAAATGT
TCCAGAACTCTGCAACGAAGAGTAGAAGAAATTAACACAGCGCTTAGAAGAAATGACACAGAGAAATGGAAGCCC
TGGAAAACTCCCTGAGATACAGATGAAGATTAGAAATTCGCGACACATTTGATGTCTGATACCGGATTACAT
GAACCGAGTGCAGAGCCCAAGCTCAGGCTATTGTTAAATCAATAATGTTGTGAAGTAAACCAATCAGTACTGA
GAAACCTGGTTTGGCAGACGAAAGACAAAGATATACACTAACTTGATATAAATTTATCTAGGAAAAAAATCTC
TCAGAAATCTAAGATGAATTTACACAGGTGAGAAATGAATAGCTATGCAAGGTTATTTGTAATATCTGTGGACAC
AACTGTCTCTGCTCTCCTGCTTGTGTGCAATCTCATTGACTATACGATAAGTTTGCACAGCTTCTACTT
CTGTAGAACACTGGCCATAGGAATGCTGTTTTTTGTACTGGACTTACCTTGATATATGATATGGAATGTATG
CATAAAACTCATAGGACATGTACTTTGTGGAAACAGTGGATTTTATACATATTAATAATTCACCACTTCAG

FIGURE 15

MEKMLAGCFLILGQIVLLPAEARESRGRSISRGRHARTHPTQALLESSCENKRADLVFII
DSSRSVNTHDYAKVKEFIVDILQFLDIGPDVTRVGLLQYGSTVKNEFSLKTPKRKSEVERAV
KMRHRLSTGTMGLAIQYALNIAFSEAEGARPLRENVPVIMIVTDGRPDQDSVAEVAAKARD
TGILIFAIGVGQVDFNTLKSIGSEPHEDHVFLVANFSQIETLTSTVFQKCLKTAHMCSTLEHN
CAHFCINIPGSYVCRCKQGYILNSDQTTCRIQDLCAMEDHNCEQLCVNVPGSFVCQCYSGYA
LAEDGKRCVAVDYCASENHGCEHECVNADGSYLCQCHEGFALNPDEKTCRINYCALNKPQC
EHECVNMEESSYYCRCHRGYTLDPNGKTCRSVDHCAQQDHGCEQLCLNTEDSFVCQCSEGFIL
NEDLKTCSRVDYCLLDHGCSEYSCVNMDRSFACQCPGHHVLRSDGKTCAKLSDSCALGDHGCE
HSCVSSEDSFVCQCFEGYILREDGKTCRRKDVCAIDHGCHEHICVNSDDSYTCECLBGFRLA
EDGKRCRRKDVCKSTHHGCEHICVNNNGNSYICKSEGFVLAEDGRRCKKCTEGPIDLVFVID
GSKSLGEENFEVVKQFVTGIIIDSLTISPKAARVGLLQYSTQVHTEFTLRNFSAKDMKKAVA
HMKYMGKGSMTGLALKHMFRSFTQGEGARPLSTRVPRAAIVFTDGRAQDDVSEWAKAKAN
GITMYAVGVGKAIEEELQBIASEPTNKHLFYAEDFSTMDIEISEKLKKGICEALESDGRQDS
PAGELPKTVQQPTSESEPTVINIQDLLSCSNFAVQHRYLFEEDNLLRSTQKLSHSTKPSGSL
EEKHDQCKCENLIMFQNLANEVVRKLTQRLEEMTQRMEALENRLRYR

Signal peptide:

amino acids 1-23

N-glycosylation site.

amino acids 221-225

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 115-119, 606-610, 892-896

Casein kinase II phosphorylation site.

amino acids 49-53, 118-122, 149-153, 176-180, 223-227, 243-247,
401-405, 442-446, 501-505, 624-628, 673-677, 706-710, 780-784,
781-785, 819-823, 866-870

N-myristoylation site.

amino acids 133-139, 258-264, 299-305, 340-346, 453-459, 494-500,
639-645, 690-696, 752-758, 792-798

Amidation site.

amino acids 314-318, 560-564, 601-605

Aspartic acid and asparagine hydroxylation site.

amino acids 253-265, 294-306, 335-347, 376-388, 417-423, 458-464,
540-546, 581-587

FIGURE 16

GGAGCCGCCCTGGGTGTGTCAGCGGCTCGGCTCCCGCGCACGCTCCGGCCGTCGCGCAGCCTCG
GCACCTGCAAGTCCGTGCGTCCCGCGGCTGGCGCCCTGACTCCGTCCCGGCCAGGGAGGGC
CATGATTTCCTCCCGGGGCCCCCTGGTGACCAACTTGCTGCGGTTTTTGTTCCTGGGGCTGA
GTGCCCTCGCGCCCCCTCGCGGGCCAGCTGCAACTGCACTTGCCCGCCAAACCGTTGTCAG
GCGGTGGAGGGAGGGGAAAGTGGTGCTTCAGCGTGTTACACCTTGACGCGGGAGGTGTCTTC
ATCCAGCCATGGGAGGTGCCCTTTGTGATGTGGTTCTTCAAACAGAAAGAAAAGGAGGATC
AGGTGTTGTCTACATCAATGGGGTCAACAAGCAAACTGGAGTATCCTTGGTCTACTCC
ATGCCCTCCCGGAACCTGTCCCTGCGGCTGGAGGGTCTCCAGGAGAAGACTCTGCCCCCTA
CAGCTGCTCCGTGAATGTGAAGACAAAAGGCAAACTAGGGGCCACAGCATCAAAACCT
TAGAACTCAATGTACTGGTTCCTCCAGCTCCTCCATCCTGCCGTCTCCAGGGTGTGCCCCAT
GTGGGGGCAAAACGTGACCTGAGCTGCCAGTCTCCAAGGAGTAAGCCCGCTGTCCAATACCA
GTGGGATCGGCAGCTTCATCCTTCAGACTTCTTTGCACCAGCATTAGATGTCTATCCGTG
GGTCTTTAAGCCTCACCAACCTTTCGTCTTCCATGGCTGGAGTCTATGTCTGCAAGGCCAC
AATGAGGTGGGCACTGCCAATGTAATGTGACGCTGGAAGTGAGCACAGGGCCTGGAGCTGC
AGTGGTTGTCTGGAGCTGTTGTGGGTACCCTGGTTGGACTGGGGTTGTCTGGCTGGGCTGGTCC
TCTTGTAACACCGCCGGGGCAAGGCCCTGGAGGAGCCAGCCAATGATATCAAGGAGGATGCC
ATTGCTCCCGGACCTGCCCTGGCCCAAGAGCTCAGACACAATCTCCAAGAATGGGACCTT
TTCCTCTGTACCTCCGCACGAGCCCTCCGGCCACCCCATGGCCCTCCAGGCCTGGTGCAT
TGACCCCCACGCCAGTCTCTCCAGCCAGGCCTGCCCTACCAAGACTGCCACGACAGAT
GGGGCCCAACCTCAACCAATATCCCCCATCCCTGGTGGGGTTTCTTCTCTGGCTTGAGCCG
CATGGGTGCTGTGCCTGTGATGGTGCCCTGCCAGAGTCAAGCTGGCTCTCTGGTATGATGAC
CCCACCACTCATTGGCTAAAGGATTTGGGGTCTCTCCTTCTCTATAAGGGTCACCTCTAGCAC
AGAGGCCTGAGTCATGGGAAAGAGTCACACTCCTGACCCTTAGTACTCTGCCCCACCTCTC
TTTACTGTGGGAAAACCTCTCAGTAAGACCTAAGTGTCCAGGAGACAGAAGGAGAAGAGGA
AGTGGATCTGGAATTGGGAGGAGCCTCCACCCACCCCTGACTCCTCCTTATGAAGCCAGCTG
CTGAAATTAGCTACTACCAAGAGTGAGGGGCAGAGACTTCAGTCACTGAGTCTCCAGGC
CCCTTGATCTGTACCCACCCCTATCTAACACCACCCCTGGCTCCCACTCCAGCTCCCTGT
ATTGATATAACCTGTGAGGCTGGCTTGGTTAGGTTTACTGGGGCAGAGGATAGGGGAATCTC
TTATTAATAACTAACATGAATATGTGTTGTTTTCATTGCAAATTTAAATAAAGATACATAA
TGTTTGATGAAAAA

FIGURE 17

MISLPGPLVTNLLRFLFLGLSALAPPSRAQLQLHLPANRLQAVEGGEVVLPAWYTLHGEVSS
SQPWEVPFVMWFFKQKEKEDQVLSYINGVTTSKPGVSLVYSMPSRNLSLRLEGLQEKDSGPY
SCSVNVQDKQGKSRGHSIKTLELNVLVPPAPPSCRLOGVPHVGANVTLSQCQSPRSKPAVQYQ
WDRQLPSFQTFPAPALDVIRGSLSLTNLSSSMAGVYVCKAHNEVGTAQCNVTLEVSTGPGAA
VVAGAVVGTTLVGLGLLAGLVLLYHRRGKALEEPANDIKEDAIAPRTLWPWPKSSDTISKNGTL
SSVTSARALRPFHGPPRPALTPTPSLSSQALPSPRLPTTDGAHPQPISSIPGGVSSSGLSR
MGAVPVMVPAQSQAGSLV

Signal peptide:

amino acids 1-29

Transmembrane domain:

amino acids 245-267

N-glycosylation site.

amino acids 108-112, 169-173, 213-217, 236-240, 307-311

N-myristoylation site.

amino acids 90-96, 167-173, 220-226, 231-237, 252-258, 256-262,
262-268, 308-314, 363-369, 364-370

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 164-175

FIGURE 18

CGCCACCACTGCGGCCACCGCCAAATGAAACGCCTCCCGCTCCTAGTGGTTTTTTCCACTTTG
TTGAATTGTTCCCTATACTCAAAATTGCACCAAGACACCTTTGTCTCCCAAAATGCAAAATGTGA
AATACGCAATGGAATTGAAGCCTGCTATTGCAACATGGGATTTTCAGGAAATGGTGTACAA
TTTGTGAAGATGATAATGAATGTGGAAATTTAACTCAGTCCTGTGGCGAAAATGCTAATTGC
ACTAACACAGAAGGAAGTTATTATTGTATGTGTGTACCTGGCTTCAGATCCAGCAGTAACCA
AGACAGGTTTTATCACTAATGATGGAACCGCTCTGTATAGAAAATGTGAATGCAAACTGCCATT
TAGATAATGTCTGTATAGCTGCAAAATTAATAAACTTTAACAAAAATCAGATCCATAAAA
GAACCTGTGGCTTTGCTACAAGAAAGTCTATAGAAATTCGTGACAGATCTTTTACCACAGA
TATAATTACATATATAGAAATATTAGCTGAATCATCTTCATTACTAGGTTACAAGAACACA
CTATCTCAGCCAAGGACACCTTTCTAACTCAACTCTTACTGAATTTGTAAAAACCGTGAAT
AATTTTGTTCAAAGGGATACATTTGTAGTTTGGGACAAGTTATCTGTGAATCATAGGAGAAC
ACATCTTACAAAACCTCATGCACACTGTTGAACAAGCTACTTTAAGGATATCCAGAGCTTCC
AAAAGACCACAGAGTTTGATACAAATTCACCGATATAGCTCTCAAAGTTTTCTTTTTTGAT
TCATATAACATGAAACATATTTCCTCATATGAATATGGATGGAGACTACATAAAATATATT
TCCAAAGAGAAAAGCTGCATATGATTCAAATGGCAATGTTGCAGTTGCATTTTATATTTATA
AGAGATTGGTCTTTGCTTTTCATCATCTGACAACTTCTTATTGAAACCTCAAAATTTATGAT
AATCTGAAGAGGAGGAAAAGAGTCATATCTTCAGTAATTTTTCAGTCTCAATGAGCTCAAACCC
ACCCACATTTATGAACTTGAAAAAATAACATTTACATTAAGTCATCGAAAGGTCACAGATA
GGTATAGGAGCTATGTGCATTTTGGAAATTAACCTGATACCATGAATGGCAGCTGGTCT
TCAGAGGGCTGTGAGCTGACATACTCAAATGAGACCCACACCTCATGCCGCTGTAATCACCT
GACACATTTTGCATTTTGATGTCTCTGGTCTTCCATTGGGTATTAAGATTATAATATTC
TTACAAGGATCACTCAACTAGGAATAATTTATTCAGTGATTTGGCTTGCCATATGCATTTT
ACCTTCTGGTCTTTCAGTGAATTCAAAGCACCAGGACAACAATTCACAAAAATCTTTGCTG
TAGCCTATTTCTGTGTAACCTGTTTTTCTTGTGGGATCAATACAAATACTAATAAGCTCT
TCTGTTCATATTCGCCGACTGTACACTACTTCTTTTTAGTCTGCTTTTGATGGATGTGC
ATTGAAGGCATACATCTCTATCTCATTGTTGTGGGTGTCTATACAAAGGGATTTTGTGA
CAAGAATTTTTATATCTTTGGCTATCTAAGCCAGCCGTGGTAGTTGGATTTTCGGCAGCAC
TAGGATACAGATATTTAGGCAACAACCAAGTATGTTGGCTTAGCACCGAAAAACAATTTAT
TGGAGTTTTATAGGAACTGACATGCCTAATCATCTCTGTTAACTCTTGGCTTTTGAGTCAT
CATATACAAAGTTTTTTCGTCACTGCGGGTTGAAACCAGAAGTTAGTTGCTTTGAGAACA
TAAGGTCTGTGCAAGAGGAGCCCTCGCTCTTCTGTCTCTCGGCACCACCTGGATCTTT
GGGTTCTCCATGTTGTGCAAGCATCAGTGGTTACAGCTTACCTTCAAGTCAGCAATGC
TTTTCCAGGGGATGTTCAATTTTTATTCTGTGTGTTTTATCTAGAAAGATTCAAGAAGAT
ATTACAGATTTGTTCAAAATGTCCCTGTTGTTTTGGATGTTTAAAGTAAACATAGAGAATG
TGGATTAATTACAAGTGCACAAAAATAAAAAATCCAAGCTGTGGATGACCAATGTATAAAAA
TGACTCATCAAATTTCAATATTATTAACCTAGACAAAAAGTATTTTAAATCAGTTTTTCT
GTTTATGCTATAGGAAGCTAGATAAATAGGTAAATATGATCATATAGATATATACTATGT
TTTTCTATGTGAAATAGTTCTGTCAAAAAATAGTATTGCAGATATTTGGAAGTAATTGGTTT
CTCAGGAGTGATATCACTGCACCCAGGAAAGATTTCTTTCTAACACGAGAAGTATATGAA
TGTCTTCAAGTAAACCACTGGCTGTATATTTCTGTGACTCGTGTGGCTTTGAACTAGTCC
CTTACCACCTCGGTATGAGCTCCATTACAGAAAGTGAACATAAGAGAATGAAGGGGCAGA
ATATCAACAGTGAAGGGAATGATAAGATGTATTTGAATGAACCTGTTTTTCTGTAGAC
TAGCTGAGAAATTTGACATAAAATAAGAAATGAAGAAACACATTTTACCATTTTGTGAA
TTGTTCTGAACCTTAAATGTCCATAAAACCACTTAGACTTCTGTTGTGTAATCTGTTCTT
TTTCTAATATTCTAAAAAAGGTTTACCTCCACAATTGAAAAAAGGTTTAAAAAAGGTTT
AAAAAAGGTTTAAAAAAGGTTTAAAAAAGGTTTAAAAAAGGTTTAAAAAAGGTTTAAAAAAGGTTT

CGCCACCACTGCGGCCACCGCCAAATGAAACGCCTCCCGCTCCTAGTGGTTTTTTCCACTTTG

FIGURE 19

MKRLPLLVVVFSTLLNCSYTNCTKTPCLPNAKCEIRNGIEACYCNMGFSGNGVTICEDDNEC
GNLTQSCGENANCTNTEGSYYCMCVPGFRSSSNQDRFITNDGTVCIEENVNANCHLDNVCIAA
NINKTTLTKIRSIKEPVALLQEVYRNSVTDLSPTDIIITYEILAESSSLLGYKNNTISAKDTL
SNSSTLTFTFVKTVNNFVQORDTFVVWDKLSVNHRRTHLTKLMHTVEQATLRISQSQFQKTTTFEDT
NSTDIALKVFFFDSDYNMKHIHPHMNDGDYINIFPKRKAAYDSNGNVAVAFLYYKSIGPLLS
SSDNFLLKPQNYDENSEEEERVISSVISVSMSSNPPTLYELEKITFTLSHRKVTDYRSLCAF
WNYSPDTMNGSWSSSEGCELTYSNETHTSCRCNHLTHFAILMSSGSPSIGIKDYNILTRITQLG
IIISLICLAICIFTFWFFSEIQSTRTTTHKNLCCSLFLAELVFLVGINTNTNKLFCSEIIAGL
LHYFFLAFAFWMCIEGIIHLYLIVVGVYINKGFLHKNFYIFGYLSPAVVVGFSAAALGYRYYGT
TKVCWLSTENNFIWFSFIGPACLIILVNLLAFGVIIYKVFRTAGLKPEVSCFENIRSCARGA
LALLFLGLTTWIFGVLHVHVASVVTAYLFTVSNAFQGMFIFLFLCVLSRKIQEEYYRLFKNV
PCCFGCLR

Signal peptide:

amino acids 1-19

Transmembrane domain:

amino acids 430-450, 465-486, 499-513, 535-549, 573-593, 619-636,
648-664

N-glycosylation site.

amino acids 15-19, 21-25, 64-68, 74-78, 127-131, 177-181,
188-192, 249-253, 381-385, 395-399

Glycosaminoglycan attachment site.

amino acids 49-53

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 360-364

Casein kinase II phosphorylation site.

amino acids 54-58, 68-72, 76-80, 94-98, 135-139, 150-154,
155-159, 161-165, 181-185, 190-194, 244-248, 310-314, 325-329,
346-350, 608-612

Tyrosine kinase phosphorylation site.

amino acids 36-44, 669-677, 670-678

N-myristoylation site.

amino acids 38-44, 50-56, 52-58, 80-86, 382-388, 388-394,
434-440, 480-486, 521-527

Aspartic acid and asparagine hydroxylation site.

amino acids 75-87

FIGURE 20

TGGAAACATATCCTCCCTCATATGAATATGGATGGAGACTACATAAAATATATTTCCAAAGNG
AAAAGCCGGCATATGGATTCAAATGGCAATGTTGCAGTTGCATTTTTATATTATAAGAGTAT
TGGTCCCTTTGCTTTTCATCATCTGACAACTTCTTATTGAAACCTCAAAATTATGATAATTCT
GAAGAGGAGGAAAGAGTCATATCTTCAGTAATTTCAAGTCTCAATGAGCTCAAACCCACCCAC
ATTATATGAACTTGAAAAAATAACATTTACATTAAGTCATCGAAAGGTCACAGATAGGTATA
GGAGTCTATGTGGCATTTTGAATACTCACCTGATACCATGAATGGCAGCTGGTCTTCAGAG
GGCTGTGAGCTGACATACTCAAATGAGACCCACACCTCATGCCGCTGTAATCACCTGACACA
TTTTGCAATTTTGATGTCTCTGGTCTTCCATTGGTATTAAAGATTATAATATTCTTACAA
GGATCACTCAACTAGGAATAATTATTTCACTGATTTGTCTTGCCATATGCATTTTTACCTTC
TGGTTCCTCAGTGAAATTCAAAGCACCAGGA

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FIGURE 21

GCTCCAGCCAAGAACCTCGGGGCCGCTGCGCGGTGGGGAGGAGTTCCCCGAAACCCGGCCG
CTAAGCGAGGCCCTCCTCCTCCCGCAGATCCGGAACGGCCTGGGGCGGGGTACCCCGGCTGGGA
CAAGAAGCCGCGCCTGCCTGCCGCCGGGCCGGGGAGGGGGCTGGGGCTGGGGCCGGAGGCGG
GGTGTGAGTGGGTGTGTGCGGGGGCGGAGGCTTGATGCAATCCCGATAAGAAATGCTCGGG
TGCTTTGGGCACCTACCCGTGGGGCCCCGTAAGGCGCTACTATATAAGGCTGCCGGCCCCGGAG
CCGCGCGCCGCTCAGAGCAGGAGCGCTGCGTCCAGGATCTAGGGCCACGACCATCCCAACCC
GGCACTCACAGCCCCGAGCGCATCCCGGTGCGCGCCAGCCTCCCGCACCCCATCGCCGG
AGCTGCGCCGAGAGCCCCAGGGAGGTGCCATGCGGAGCGGGTGTGTGTGGTCCACGTATGG
ATCTGCGCCGCTCTGGCTGGCCGTGGCCGGGGCCCCCTCGCCTTCTCGGACGCGGGGGCC
CCACGTGCACTACGGCTGGGGCGACCCCATCCGCTGCGGCACCTGTACACCTCCGGCCCCC
ACGGGCTCTCCAGCTGCTTCTCTGCGCATCCGTGCCGACGGCGTCTGTGACTGCGCGCGGGG
CAGAGCGCGCACAGTTTGCTGGAGATCAAGGCAGTCGCTCTGCGGACCGTGGCCATCAAGGG
CGTGCAAGCGTGCGGTACCTCTGCATGGGCGCCGACGGCAAGATGCAGGGGCTGCTTCAGT
ACTCGGAGGAAGACTGTGCTTTCGAGGAGGAGATCCGCCAGATGGCTACAATGTGTAACGA
TCCGAGAAGCACCGCCTCCCGGTCTCCCTGAGCAGTGCCAAACAGCGGCAGCTGTACAAGAA
CAGAGGCTTCTTCCACTCTCTCATTTCTGCCCCATGCTGCCCATGGTCCAGAGGAGCCTG
AGGACCTCAGGGGCCACTTGGAATCTGACATGTTCTCTTCGCCCTTGGAGACCGACAGCATG
GACCCATTGGGCTTGTACCCGACTGGAGGCCGTGAGGAGTCCCAGCTTTGAGAAGTAACT
GAGACCATGCCCCGGGCTCTTCACTGCTGCCAGGGGCTGTGGTACTGCAGCGTGGGGGACG
TGCTTCTACAAGAACAGTCTGAGTCCACGTTCTGTTTAGCTTTAGGAAGAAACATCTAGAA
GTTGTACATATTCAGAGTTTTCCATTGGCAGTGCCAGTTTCTAGCCAATAGACTTGTCTGAT
CATAACATTGTAAGCCTGTAGCTTGCCAGCTGCTGCTGGGCCCCATTCTGCTCCCTCGA
GGTTGCTGGACAAGCTGCTGCACTGTCTCAGTTCGTCTGAATACCTCCATCGATGGGGAAC
TCACTTCCTTTTGGAAAAATTCTTATGTCAAGCTGAAATTCCTAATTTTTCTCATCACTTC
CCCAGGAGCAGCCAGAAGACAGGCAGTAGTTTTTAATTTAGGAACAGGTGATCCACTCTGTA
AAACAGCAGGTAAATTTCACTCAACCCCATGTGGGAATTGATCTATATCTCTACTTCCAGGG
ACCATTTTCCCTTCCCAAAATCCCTCCAGGCCAGAACTGACTGGAGCAGGCATGGCCACCAAG
GCTTCAGGAGTAGGGGAAGCCTGGAGCCCCACTCCAGCCCTGGGACAACCTTGAGAAATTTCCC
CTGAGGCCAGTTCTGTATGGATGCTGTCTGAGAATAACTTGCTGTCCCGGTGTCACTGTC
TTCCATCTCCCAGCCCCACCAGCCCTCTGCCACCTCACATGCCCTCCCCATGGATTGGGGCCT
CCCAGGCCCCCACCTTATGTCAACCTGCACATTCTGTTCAAAAATCAGGAAAGAAAAGAT
TTGAAGACCCCAAGTCTTGTCAATAACTTGCTGTGTGGAAGCAGCGGGGGAAGACCTAGAAC
CCTTTCCCAGCACTTGGTTTTTCCAACATGATATTTATGAGTAATTTATTTTGATATGTACA
TCTCTTATTTTCTTACATTATTTATGCCCCCAAATATATTTATGTATGTAAGTGAGGTTTG
TTTTGTATATTAAAAATGGAGTTTGGTTTG

FIGURE 22

MRSGCVVHVWILAGLWLAVAGRPLAFSDAGPHVHYGWDPIRLRHLYTSGPHGLSSCFLRI
RADGVVDCARGQSAHSLLEIKAVLRRTVAIKGVHSVRYLCMGADGKMQGLLQYSEEDCAFEE
EIRPDGYNVYRSEKHLPLVSLSSAKQRQLYKNRGFLPLSHFLPMLPMVFEEPEDLRGHLESD
MFSSPLETDSMDPFGLVTGLEAVRSPSF EK

Signal peptide:

amino acids 1-22

Casein kinase II phosphorylation site.

amino acids 78-82, 116-120, 190-194, 204-208

N-myristoylation site.

amino acids 15-21, 54-60, 66-72, 201-207

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 48-59

FIGURE 23

CCCAGAAGTTCAAGGGCCCCCGCCTCCTGCGCTCCTGCCGCCGGGACCCCTCGACCTCCTCA
GAGCAGCCGGCTGCCGCCCCGGGAAGATGGCGAGGAGGAGCCGCCACCGCCTCCTCCTGCTG
CTGTGCGCTACCTGGTGGTCGCCCTGGGCTATCATAAGGCCTATGGGTTTTCTGCCCAAA
AGACCAACAAGTAGTACAGCAGTAGAGTACCAAGAGGCTATTTTAGCCTGCAAAACCCAA
AGAAGACTGTTTCTCCAGATTAGAGTGGAAGAAACTGGGTCGGAGTGTCTCCTTTGTCTAC
TATCAACAGACTCTTCAAGGTGATTTTAAAAATCGAGCTGAGATGATAGATTTCATATCCG
GATCAAAAATGTGACAAGAAGTGATGCGGGGAAATATCGTTGTGAAGTTAGTGCCCCATCTG
AGCAAGGCCAAAACCTGGAAGAGGATACAGTCACTCTGGAAGTATTAGTGGCTCCAGCAGTT
CCATCATGTGAAGTACCCCTTCTGCTCTGAGTGGAACTGTGGTAGAGCTACGATGTCAAGA
CAAAGAAGGGAATCCAGCTCCTGAATACACATGGTTTAAGGATGGCATCCGTTTGCTAGAAA
ATCCCAGACTTGGCTCCCAAAGCACCAACAGCTCATACAAATGAATACAAAACCTGGAAC
CTGCAATTTAATACTGTTTCCAAACTGGACACTGGAGAATATTCCTGTGAAGCCGCAATTC
TGTTGGATATCGCAGGTGTCTTGGGAAACGAATGCAAGTAGATGATCTCAACATAAGTGGCA
TCATAGCAGCCGTAGTAGTTGTGGCCTTAGTGATTTCGTTTGTGGCCTTGGTGTATGCTAT
GCTCAGAGGAAAGGCTACTTTTCAAAGAAACCTCCTTCCAGAAGAGTAATTCTTCATCTAA
AGCCACGACAATGAGTGAAAATGTGCAGTGGCTCACGCCTGTAATCCCAGCACTTTGGAAGG
CCGCGCGCGCGGATCACGAGGTGAGGAGTTCTAGACCAGTCTGGCCAAATATGGTGAAACCC
CATCTCTACTAAAATACAAAATTAGCTGGGCATGGTGGCATGTGCCTGCAGTTCAGCTGC
TTGGGAGACAGGAGAATCACTTGAACCCGGGAGGCGGAGGTTGCAGTGAGCTGAGATCACGC
CACTGCAGTCCAGCCTGGGTAAACAGAGCAAGATTCATCTCAAAAATAAAATAAATAAATA
AATAAATACTGGTTTTTACCTGTAGAATTCTTACAATAAATATAGCTTGATATTC

FIGURE 24

MARRSRHRLLLLLLRYLVVALGYHKAYGFSAPKDQQVVTAVEYQERAILACKTPKKTVSSRLE
WKKLGRSVSFVYYQQTLCQDFKNRAEMIDFNIRIKNVTRSDAGKYRCEVSAPSEQGQNLEED
TVTLEVLVAPAVPSCEVPSSALSGTVVELRCQDKEGNPAPEYTWFKDGIRLLENPRLGQSQT
NSSYTMNTKTGTLQFNTVSKLDTGEYSCEARNSVGYYRRCPGKRMQVDDLNISGIIAAVVVVA
LVISVCGLGVCYAQRKGYSKETSFQKSNSSSKATTMSENVQWLTVPVIPALWKAAGGSRGQEF

Signal peptide:

amino acids 1-20

Transmembrane domain:

amino acids 130-144, 238-258

N-glycosylation site.

amino acids 98-102, 187-191, 236-240, 277-281

Casein kinase II phosphorylation site.

amino acids 39-43, 59-63, 100-104, 149-153, 205-209, 284-288

N-myristoylation site.

amino acids 182-188, 239-245, 255-261, 257-263, 305-311

Amidation site.

amino acids 226-230

FIGURE 25

GACATCGGAGGTGGGCTAGCACTGAAACTGCTTTTCAAGACGAGGAAGAGGAGGAGAAAGAG
AAAGAAGAGGAAGATGTTGGGCAACATTATTATTAAACATGCTCCACAGCCCGGACCCTGGGCAT
CATGCTGCTATTCTCGCAAATACTGAAGAAGCATGGGATTTAAATATTTTACTTCTTAAATAA
ATGAATTACTCAATCTCCTATGACCATCTATACATACTCCACCCTTCAAAAAGTACATCAATA
TTATATCATTAAGGAAATAGTAACCTTCTCTTCTCCAATATGCATGACATTTTGGGCAATG
CAATTGTGGCACTGGGCACTTATTTTCAGTGAAGAAAACTTTGTGGTTCTATGGCATTTCATCA
TTTGACAATGCAAGCATCTTCTTATCAATCAGCTCCTATTGAACTTACTAGCACTGACCTG
TGGAACTCCTTAAGGGCCCATACATTTCTGAAGAAGAAAGCTAAGATGAAGGACATGCCACT
CCGAATTCATGTGCTACTTTGGCCTAGCTATCACTACACTAGTACAAGCTGTAGATAAAAAAG
TGGATTGTCCACGGTTATGTACGTGTGAAATCAGGCCTTGGTTTACACCAGATCCATTTAT
ATGGAAGCATCTACAGTGGATTGTAATGATTTAGGTCTTTTAACTTTCCAGCCAGATTGCC
AGCTAACACACAGATTCTTCTCTACAGACTAACATATTGCAAAAATTGAATACTCCACAG
ACTTTCCAGTAAACCTTACTGGCCTGGATTATCTCAAAACAATTTATCTTCAGTCACCAAT
ATTAATGTAAAAAAGATGCCCTCAGCTCCTTTCTGTGTACCTAGAGGAAAAACAACTTACTGA
ATGCTCCTGAAAAATGTCTGTCGGAAGCTGAGCAACTACAAGAACTCTATATTAATCAACAAT
TGCTTTCTACAAHTTCACTTGGAGCCTTATTGGCCCTACATAAFTCTTCTGACTTCCATCTC
AATTCAAATAGATTGCAGATGATCAACAGTAAGTGGTTTGTATGCTCTTCCAAATCTAGAGAT
TCTGATGATGGGGAAAAATCCAATTATCAGAATCAAAGACATGAACCTTTAAGCCTCTTATCA
ATCTTCGACGGCTGGTTATAGCTGGTATAAACTCACAGAAATACCAGATAACGCCCTTGGTT
GGACTGGAAAACTTAGAAAGCATCTCTTTTTACGATAACAGGCTTATTAAAGTACCCCATGT
TGCTCTTCAAAAAGTTGTAATCTCAAATTTTGGATCTAAAATAAAAACTCTATTAATAGAA
TACGAAGGGGTGATTTTAGCAATATGCTACACTTAAAGAGTTGGGGATAAAATAATATGCCCT
GAGCTGATTTCCATCGATAGTCTTGTCTGGGATAAAGCTGCCAGATTTAAGAAAAATAGAAGC
TACTAACAAACCTAGATTGTCTTACATTCACCCCAATGCATTTTTCAGACTCCCCAAGCTGG
AATCACTCATGTGAACAGCAATGCTCTCAGTGCCTGTACCATGGTACCATTGAGTCTCTG
CCAAACCTCAAGGAAATCAGCATACACAGTAACCCCATCAGGTGTGACTGTGTCTATCCGTTG
GATGAACATGAACAAAACCAACATTCGATTTCATGGAGCCAGATTCACTGTTTGGCTGGACC
CACCTGAATTCGAAGTTCAGAAATGTCGGCAAGTGCAATTTTCAGGACATGATGGAATTTGT
CTCCTCTTATAGCTCCTGAGAGCTTTCTCTTAATCTAAATGTAGAAGCTGGGAGCTATGT
TTCCTTTCACTGTAGAGCTACTGCAGAACCACAGCCTGAAATCTACTGGATAACACCTTCTG
GTCAAAAACCTCTTGCTTAATACCTGCAGACAAAGTTCTATGTCCATTCTGAGGGAACTA
GATATAAATGGCGTAACCTCCAAAGAAGGGGGTTTATATACTTGATAGCAACTAACCTAGT
TGGCGCTGACTTGAAGTCTGTTATGATCAAAGTGGATGGATCTTTTCCACAAGATAACAATG
GCTCTTTGAATATTAATAAGAGATATTCAGGCCAATTCAGTTTGTGTCTCTGGAAGACA
AGTTCTAAAAATCTCAAATCTAGTGTAAATGGACAGCCTTTGTCAAGACTGAAAAATCTCA
TGTGCGCAAGTGCTCGAATACCATCTGATGTCAAGGTATATAATCTTACTCATCTGAATC
CATCAACTGAGTATAAAATTTGTATTGATATTCCCACTATCATAGAAAAACAGAAAAAA
TGTGTAATGTCAACCACCAAGGTTTGCACCCTGATCAAAAAGAGTATGAAAAAGATAATAC
CACAACACTTATGGCTGTCTTGGAGGCCTTCTGGGGATTATTGGTGTGATATGTCTTATCA
GCTGCCCTCTCCACAAATGAACGTGTGATGGTGGACAAGCATGTGAGGAATTACTTACAG
AAAGCAACCTTTGCATTAGGTGAGCTTTATCTCTCTGTATAAATCTCTGGGAAGCAGGAAA
AGAAAAAGTACATCACTGAAAGTAAAGCAACTGTTATAGGTTTACCAACAAATATGTCCT
AAAAACCACCAAGGAACCTACTCCAAAAATGAC

FIGURE 26

MKDMPLRIHVLLGLAITTLVQAVDKKVDPCRLCTCEIRPWFTPRSIYMEASTVDCNDLGLLT
FPARLPANTQIILLQTNNAIKIEYSTDFPVNLTGLDLSQNNLSSVTNINVKKMPQLLSVYLE
ENKLTPEKCLSELNLQELYINHNLLSTISPGAFIGLHNLRLHLNSNRLQMINSKWFDA
LPNLIELMIGENPIIRIKDMNFKPLINLRSLVIAGINLTEIPDNALVGLLENLESISFYDNRL
IKVPHVALQKVVNLFKLDLNKNPINRIRRGDFSNMLHLKELGINNMPELISIDSLAVDNLPD
LRKIEATNNPRLSYIHPNAFFRLPKLESIMLNSNALSYHGTIESLPNLKEISIHNPIRC
DCVIRWMNMKNINIRFMEPDSLFCVDPPEFQGGQNVVRQVHFQVHFRDMMETCLPLIAPESFPSNLNV
EAGSYVSFHCRTAEPQPEIYWIITPSGQKLLPNTLTDKFVYHSECTLDINGVTPKEGGLYTC
IATNLVGADLKSVMIKVDGSFPQDNNGSLNIKIRDIQANSVLVSWKASSKILKSSVKWTAFAV
KTENSHAAQSARIPSDVKVYNLTHLNPSTEYKICIDIPTIYQKNRKKCVNVTTKGLHPDQKE
YEKNNTTTLMACLGGLGIIGVICLISCLSPENMCDGGHSYVRNYLQKPTFALGELYPPLIN
LWEAGKEKSTSLKVKATVIGLPTNMS

Signal sequence:

amino acids 1-22

Transmembrane domain:

amino acids 633-650

N-glycosylation site.

amino acids 93-97, 103-107, 223-227, 382-386, 522-526, 579-583,
608-612, 624-628, 625-629

Casein kinase II phosphorylation site.

amino acids 51-55, 95-99, 242-246, 468-472, 487-491

Tyrosine kinase phosphorylation site.

amino acids 570-579

N-myristoylation site.

amino acids 13-19, 96-102, 158-164, 221-227, 352-358, 437-443,
491-497, 492-498, 634-640, 702-708

Cell attachment sequence.

amino acids 277-280

FIGURE 27

CCCCGGGACTGGCGCAAGGTGCCAAGCAAGGAAAGAAATAATGAAGAGACACATGTGTTAG
CTGCAGCCTTTTGA AACACGCAAGAAGGAAATCAATAGTGTGGACAGGGCTGGAACCTTTAC
CACGCTTGTGTGGAGTAGATGAGGAATGGGCTCGTGATTATGCTGACATTCAGCAATGAATCT
GGTAGACCTGTGGTTAACCCGTTCCCTCTCCATGTGTCTCTCTACAAAGTTTGTCTCTTA
TGATACTGTGCTTTTATTCTGCCAGTATGTGTCCCAAGGGCTGTCTTTGTTCTTCTCTGGG
GGTTTAAATGTCACCTGTAGCAATGCAAATCTCAAGGAAATACCTAGAGATCTTCTCTCTGA
AACAGTCTTACTGTATCTGGACTCCAATCAGATCACATCTATTCCCAATGAAATTTTAAAGG
ACCTCCATCAACTGAGAGTTCTCAACCTGTCCAAAAATGGCATTGAGTTTATCGATGAGCAT
GCCTTCAAAGGAGTAGCTGAAACCTTGCAGACTCTGGACTTGTCCGACAATCGGATTCAAAG
TGTGCACAAAAATGCCTTCAATAACCTGAAGGCCAGGGCCAGAATTGCCAACACCCCTGGC
ACTGCGACTGTACTCTACAGCAAGTTCTGAGGAGCATGGCGTCCAATCATGAGACAGCCCAC
AACGTGATCTGTAAAAACGTCCGTGTTGGATGAACATGCTGGCAGACCATTCCTCAATGCTGC
CAACGACGCTGACCTTTGTAAACCTCCCTAAAAAACTACCGATTATGCCATGCTGGTCACTA
TGTTTGGCTGGTTCACTATGGTGATCTCATATGTGGTATATTATGTGAGGCAAAATCAGGAG
GATGCCCGGAGACACCTCGAATACTTGAAATCCCTGCCAAGCAGGCAGAAGAAAGCAGATGA
ACCTGATGATATTAGCACTGTGGTATAGTGTCCAACTGACTGTCTATTGAGAAAGAAAGAAA
GTAGTTTGCGATTGCAGTAGAAATAAGTGGTTTACTTCTCCCATCCATTGTAAACATTTGAA
ACTTTGTATTTTCACTTTTGTGAATTATGCCACTGCTGAACTTTAAACAACTACAACA
TAAATAATTTGAGTTTAGGTGATCCACCCCTTAATTGTACCCCGATGGTATATTTCTGAGT
AAGCTACTATCTGAACATTAGTTAGATCCATCTCACTATTTAATAATGAAATTTATTTTTT
AATTTAAAGCAAATAAAAGCTTAACTTGAACCATGGGAAAAAAAAAAAAAAAAAAAAACA

FIGURE 28

MNLVDLWLTRSLSMCILLQSFVLMILCFHSASMC PKGCLCSSSGGLNVTC SNANLKEIPRDL
PPETVLLYLD SNQITSIPNEIFKDLHQLRVLNLSKNGIEFIDEHAFKGVAETLQTLDSLSDNR
IQSVHKNAFN NLKARARIANNPWHCDCTLQQVLRSMASNHETAHN VICKTSVLDEHAGRPF L
NAANDADLCNL PKKT TDYAMLVTMFGWFTMVISYV VYVRQNQEDARRHLEYL KSLPSRQKK
ADEPDDISTVV

Signal sequence:

amino acids 1-33

Transmembrane domain:

amino acids 205-220

N-glycosylation site.

amino acids 47-51, 94-98

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 199-203

Casein kinase II phosphorylation site.

amino acids 162-166, 175-179

N-myristoylation site.

amino acids 37-43, 45-51, 110-116

FIGURE 29

ACCGAGCCGAGCGGACCGAAGGCGCGCCCGAGATGCAGGTGAGCAAGAGGATGCTGGCGGGG
GGCGTGAGGAGCATGCCAGCCCCCTCCTGGCCTGCTGGCAGCCCATCCTCCTGCTGGTGCT
GGGCTCAGTGCTGTCTCAGGCTCGGCCACGGGCTGCCCGCCCCGCTGCGAGTGCTCCGCCCAGG
ACCGCGCTGTGCTGTGCCACCGCAAGTGCTTTGTGGCAGTCCCCGAGGGCATCCCCACCGAG
ACGCGCCTGCTGGACCTAGGCAAGAACCAGCATCAAACCGCTCAACACGAGACGAGTTTCGCCAG
CTTCCCGCACCTGGAGGAGCTGGAGCTCAACGAGAAACATCGTGAGCGCCGTGGAGCCCGGCG
CCTTCAACAACCTCTTCAACCTCCGGACGCTGGGTCTCCGCAGCAACCGCCTGAAGCTCATC
CCGTAGGCGTCTTCACTGGCCTCAGCAACCTGACCAAGCAGGACATCAGCGAGAACAAAGT
CGTTATCCTACTGGACTACATGTTTCAGGACCTGTACAACCTCAAGTCACTGGAGGTTGGCG
ACAAATGACCTCGTCTACATCTCTCACCGCGCCTTCAGCGGGCCTCAACAGCCTGGAGCAGCTG
ACGCTGGAGAAATGCAACCTGACCTCCATCCCCACGAGGCGCTGTCCCACTGCACGCGCT
CATCGTCTCTGAGGCTCCGGCACCTCAACATCAATGCCATCCGGGACTACTCCTTCAAGAGGC
TGTACCGACTCAAGGTCTTGGAGATCTCCCACTGGCCCTACTTGGACACCATGACACCCAAC
TGCCTCTACGGCCTCAACCTGACGTCCCTGTCCATCACACACTGCAATCTGACCGCTGTGCC
CTACCTGGCCGTCGCCACCTAGTCTATCTCCGCTTCTCTCAACCTCTCTACAACCCCATCA
GCACCAATTGAGGGCTCCATGTTGTCATGAGCTGCTCCGGCTGCAGGAGATCCAGCTGGTGGGC
GGGCAGCTGGCCGTGGTGGAGCCCTATGCCCTTCCGCGGCTCAACTACCTGCGCGTGTCAA
TGTCTCTGGCAACAGCTGACCACACTGGAGGAATCAGTCTTCCACTCGGTGGGCAACCTGG
AGACACTCATCTGGACTCCAACCCGCTGGCCTGCGACTGTGCGCTCCTGTGGGTGTTCCGG
CGCCGCTGGCGGCTCAACTTCAACCCGGCAGCAGCCACGTGCGCCACGCCCCAGTTTGTCCA
GGGCAAGGAGTTCAAGGACTTCCCTGATGTGCTACTGCCCAACTACTTCACTGCGCCGGC
CCCGCATCCGGGACCGCAAGGCCAGCAGGTGTTTGTGGACGAGGGCCACAGGTGCAAGTTT
GTGTGCCGGGCCGATGGCGACCCGCGCCCGCCCATCCTCTGGCTCTACCCCCGAAAGCACT
GGTCTCAGCCAAGGCAATGGCGGCTCACAGTCTTCCCACTGTCAGCTGGAGGTGCGCT
ACGCCCAGGTACAGGACAACGGCACGTACCTGTGCTATCGCGGCCAACCGGGCGGCAACGAC
TCCATGCCCGCCCACTGCATGTGCGCAGCTACTCGCCGACTGGCCCCATCAGCCCCAACAA
GACCTTTCGCTTTCATCTCCAACAGCCGGGCGAGGGAGAGGCCAACAGCACCCGCGCCACTG
TGCTTTTCCCCTTCGACATCAAGACCTCATCATCGCCACCAACCATGGGCTTCATCTCTTTC
CTGGCGCTCGTCTCTTCTGCGCTGGTGTGCTGTTTCTCTGGAGCCGGGGCAAGGGCAACAC
AAAGCACAACATCGAGATCGAGTATGTGCCCGAAAGTCGGACGCAAGGCATCAGTCCCGCG
ACGCGCCCCGCAAGTTCAACATGAAGATGATATGAGGCGCGGGCGGGGGGCAAGGACCCCG
GGCGGCCGGGCAAGGGGAAGGGGCTGGTCGCCACCTGCTCACTCTCCAGTCTTCCACCTC
CTCCCTACCCCTTCTACACACGTTCTCTTCTCCCTCCCGCTCCGTCCCCTGCTGCCCCCG
CCAGCCCTCACCACCTGCGCTCCTTCTACCAGGACCTCAGAAGCCCAGACCTGGGGACCCCA
CCTACACAGGGGCAATTGACAGACTGGAGTTGAAAGCCGACGAAACGACACGCGGCGAGAGTCA
ATAATTCAATAAAAAAGTTACGAACTTCTCTGTAACTTGGGTTTCAATAATTATGGATTTT
TATGAAACTTGAATAATAAAAAAGAAAAAACTAAAAA

FIGURE 30

MQVSKRMLAGGVSRMSPSPLLACWQPILLVLGSLVSGSATGCPPRCECSAQDRAVLCHRKCF
VAVPEGIPTETRLDLGKNRIKTLNQDEFASFPHLEELNENI VSAVEPGAFNNLFLNLRTL
GLRSNRLKLIPLGVFTGLSNLTQDISENKIVILLDYMFDLYNLKSLEVGDNDLVYISHRA
PFGLSLSLEQLTLEKCNLTSIPTALSHLHGLIVLRRLRLNINAIIRDYSFKRLYRLKVLKLEISH
WPYLDTMTPNCLYGLNLTSLSITHCNLTAVPYLAVRHLVYLRFLNLNLSYNPISTIEGSMLEL
LRLQEIQLVGGQLAVVEPYAFRGLNYLRVLNVSGNQLTTLEESVFHSVGNLETILDSNPLA
CDCRLLWVFRRRWRLNFNRRQOPTCATPEFVQGKEFKDFPDVLLPNYFTCRRARIRDRKAQQV
FVDEGHTVQFVCRADGDPPIAILWLSPRKHLVSAKSNGRITVFPDGTLEVRYAQVQDNNGTYL
CIAANAGGNDSPMAHLHVRYSYSPDWPHQPNKTFAFISNQPGEGEANSTRATVPFPFDIKTLI
IATTMGFISFLGVVLFCLVLLFLWSRGKGNTHNIEYVPRKSDAGISSADAPRKFNMKMI

Signal sequence:

amino acids 1-41

Transmembrane domain:

amino acids 556-578

N-glycosylation site.

amino acids 144-148, 202-206, 264-268, 274-278, 293-297, 341-345,
492-496, 505-509, 526-530, 542-546

Casein kinase II phosphorylation site.

amino acids 49-53, 108-112, 146-150, 300-304, 348-352, 349-353,
607-611

Tyrosine kinase phosphorylation site.

amino acids 590-598

N-myristoylation site.

amino acids 10-16, 32-38, 37-43, 113-119, 125-131, 137-143,
262-268, 320-326, 344-350, 359-365, 493-499, 503-509, 605-611

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 32-43

FIGURE 31

CCCACGCGTCCGCACCTCGGCCCGGGCTCCGAAGCGGCTCGGGGCGCCCTTTTCGGTCAAC
ATCTAGTCCACCCCTCCCATCCCCAGCCCCGGGATTACGGCTCGCCAGCGCCAGCC
AGGGAGCCGGCCGGGAAGCGCGATGGGGGCCCCAGCCGCTCGCTCCTGCTCCTGCTCTG
TGTTCCGCTGCTGCTGGGCGCCCGCGGGGCCAACCTCTCCAGGACGACAGCCAGCCCTGG
ACATCTGATGAAACAGTGGTGGCTGGTGGCACCGTGGTGTCTCAAGTGCCAAGTGAAAGATCA
CGAGGACTCATCCTTGCAATGGTCTAACCTGCTCAGCAGACTCTCTACTTTGGGGAGAAGA
GAGCCCTTCGAGATAATCGAATTACGCTGGTTACCTCTACGCCCCACGAGCTCAGCATCAGC
ATCAGCAATGTGGCCCTGGCAGACGAGGGCGAGTACACCTGCTCAATCTTCACTATGCCTGT
GCGAACTGCCAAGTCCCTCGTCACTGTGCTAGGAATTCCACAGAAGCCCATCATCACTGGTT
ATAAATCTTTACGGGAAAAAGACACAGCCACCTAACTGTCACTCTCTGGGAGCAAG
CCTGCAGCCCGGCTCACCTGGAGAAAGGGTGACCAAGAACTCCACGGAGAACCACCCGCAT
ACAGGAAGATCCCAATGGTAAAACCTTCACTGTACGAGCTCGGTGACATTCAGGTTACCC
GGGAGGATGATGGGGCGAGCATCGTGTGCTCTGTGAACCATGAATCTCTAAAGGGAGCTGAC
AGATCCACCTCTCAACGCATTGAAGTTTATACACACCAACTGCGATGATTAGGCCAGACCC
TCCCATCCTCGTGAGGGCCAGAAGCTGTTGCTACACTGTGAGGGTCGCGGCAATCCAGTCC
CCCAGCAGTACCTATGGGAGAAGGAGGGCAGTGTGCCACCCCTGAAGATGACCCAGGAGAGT
GCCCTGATCTTCCCTTTCTCAACAAGAGTGACAGTGGCACCTACGGCTGCACAGCCACCAG
CAACATGGGCAGCTACAAGGCCTACTACACCTCAATGTTAATGACCCAGTCCGGTGCCCT
CCTCCTCCAGCACCTACCAGCCCATCATCGTGGGATCGTGGCTTTCAITGTCTTCTGCTG
CTCATCATGCTCATCTTCTTGGCCACTACTTGATCCGGCACAAAGGAACCTACCTGACACA
TGAGGCAAAAGGCTCCGACGATGTCTCCAGACGCGGACACGGCCATCATCAATGCAGAAGGCG
GGCAGTCAGGAGGGGACGACAAGAAGGAATATTTTCATCTTAGAGGCGCCTGCCCACTTCTGC
GCCCCCAGGGGCCCTGTGGGACTGCTGGGGCCGTACCAACCCGGACTTGTAACAGAGCAA
CCGACAGGGCCGCCCCCTCCGCTTGCTCCAGCCACCCACCCCTGTACAGAATGTCTGC
TTTGGGTGCGGTTTGTACTCGGTTTGAATGGGGAGGAGGGCGGGGGAGGGGAGGG
TTGCCCTCAGCCCTTTCCGTTGGCTTCTCTGCATTGGGTTATTATTATTTTGTAAACATCC
CAAAATCAAATCTGTCTCCAGGCTGGAGAGGCAGAGCCCTGGGGTGAGAAAAAGCAAAAAACA
AACAAAAACA

FIGURE 32

MGAPAASLLLLLLFACCWAPGGANLSQDDSQPWTSDETVVAGGTVVVKCQVKDHEDSSLQW
SNPAQQOTLYFGEKRALRDNRILVTSTPHELSSISINVALADEGEYTCSTFTMPVRTAKSLV
TVLGIPQKPIITGYKSSLREKDTATLNCQSSGSKPAARLTWRKGDQELHGEPTRIQEDPNGK
TFTVSSSVTFQVTREDDGASIVCSVNHESLKGADRSTSQRIEVLYTPTAMIRPDPPHPREGQ
KLLHLCEGRGNFVPQQYLWEKEGSPPLKMTQESALIFPFLNKSDSGTYGCTATSNMGSYKA
YYTLNVNDPSPVPSSSSSTYHAIIGGIVAFIVFLLLIIMLIPLGHYLIIRHKGTYLTHEAKGSDD
APDADTAIINAEGGQSGGDDKKEYFI

Signal sequence:

amino acids 1-20

Transmembrane domain:

amino acids 331-352

N-glycosylation site.

amino acids 25-29, 290-294

Casein kinase II phosphorylation site.

amino acids 27-31, 35-39, 89-93, 141-145, 199-203, 388-392

N-myristoylation site.

amino acids 2-8, 23-29, 156-162, 218-224, 295-301, 298-304,
306-310, 334-340, 360-364, 385-389, 386-390

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 7-18

FIGURE 33

GGGGGTTAGGGAGGAAGGAATCCACCCCCACCCCCCAAACCCCTTTTCTTCTCCTTTCTCTGG
CTTCGGACATTTGGAGCACATAATGAACCTGAATTTGTCTGTGGCGAGCAGGATGGTGCCTG
TTACTTTTGTGATGAGATCGGGGATGAATTTGCTCGCTTTAAAAATGCTGCTTTGGATTCTGTT
GCTGGAGACGTCCTTTTGTTTTGGCCGCTGGAAACGTTACAGGGGACGTTTGCAAAGAGAAGA
TCTGTTCTCTGCAATGAGATAGAAGGGACCTACACGTAGACTGTGAAAAAAGGGCTTCACA
AGCTCGACGCGTTTCACTGCCCCGACTTCCAGTTTACCATTATTCTGTCATGGCAATTC
CCTCACCTGCATTTTCCCTAATGAGTTCGCTAACTTTTATAATGCGGTTAGTTTGCAATGG
AAAAAATGCGCTTGCATGAATCGTTCCGGGGCTTTCTGCGGCTGCAGCTGGTGAAAGG
CTGCACATCAACAACAAGATCAAGTCTTTTCGAAAGCAGACTTTTCTGGGGCTGGACGA
TCTGGAATATCTCCAGGCTGATTTTAATTTATTACGAGATATAGACCCGGGGGCTTCCAGG
ACTTGAACAAGCTGGAGGTCTCATTTTAAATGACAATCTCATCAGCACCTTACCTGCCAAC
GTGTTCCAGTATGTGCCCATCACCCACCTCGACCTCCGGGGTAACAGGCTGAAACGCTGCC
CTATGAGGAGGTCTTGGAGCAATCCCTGGTATTGCGGAGATCCTGCTAGAGGATAACCCCT
GGGACTGCACCTGTGATCTGCTCTCCCTGAAAGAATGGCTGGAAAAACATTTCCCAAGAATGCC
CTGATCGGCAGAGTGGTCTGCGAAGCCCCACAGACTCGAGGTAAGACCTCAATGAAGAAC
CAGCGAACGAGCTTGTGTCTTTTGA AAAACCGAGTGGATTCTAGTCTCCGGGCTCCCTTG
CCCAAGAAGAGACCTTTGCTCCTGGACCCCTTGCCAACTCCTTTCAAGACAAATGGGCAAGAG
GATCATGCCACACAGGGTCTGCTCCAAACGGAGGTACAAAGATCCCAGGCAACTGGCAGAT
CAAAATCAGACCCACAGCAGCGATAGCGACGGTAGCTCCAGGAACAAACCTTAGCTAACA
GTTTACCTTGCCCTGGGGGCTGCAGCTGCGACCATCCAGGTCGGGTTTAAAGATGAAC
TGCAACAACAGGAACGTGAGCAGCTTGGCTGATTGAAGCCCAAGCTCTCTAACGTGCAGGA
GCTTTTCCACAGAGATAACAAGATCCACAGCATCCGAAATCGCACTTTGTGGATTACAAGA
ACCTCATCTGTGGATCTGGGCAACAATAACATCGCTACTGTAGAGAAACAACCTTTCAAG
AACCTTTTGGACCTCAGGTGGCTATACATGGATAGCAATTACTGTGACACGCTGTCCCGGGA
GAAATTCGCGGGGCTGCAAAACCTAGAGTACCTGAACGTGGAGTACAACGCTATCCAGCTCA
TCTCTCCCGGGCACTTTCAATGCCATGCCAAACTGAGGATCCTCATTCTCAACAACAACCTG
CTGAGGTCCCTGCCCTGTGGACGTGTTGCTGGGGTCTCGCTCTTAAACTCAGCCTGCAACA
CAATTACTTATGTACTCTCCCGTGGCAGGGGTGCTGGACCAGTTAACTCCTATCATCCAGA
TAGACCTCCACGGAAACCCCTGGGAGTGCTCTGCACAATTGTGCCCTTCAAGCAGTGGGCA
GAACGCTTGGGTTCCGAAGTGCTGATGAGCGACCTCAAGTGTGAGACGCCGCTGAACCTCTT
TAGAAAGGATTTTCATGCTCCTCTCCAATGACGAGATCTGCCCTCAGCTGTACGCTAGGATCT
CGCCACGTTAACTTCGCACAGTAAAAACAGCACTGGGTTGGCGGAGACCGGGACGCATCC
AACTCCTACCTAGACACCAGCAGGGTGTCCATCTCGGTGTTGGTCCCGGACTGCTGCTGGT
GTTTGTACCTCCGCTTACCGTGGTGGGCTGCTCGTGTATTCTGAGGAACCGAAAGC
GGTCCAAAGAGACGAGATGCCAACTCCTCCGCTCCGAGATTAACTCCCTACAGACAGTCTGT
GACTCTTCTACTGGCACAATGGGCCTTACAACGCAGATGGGGCCACAGAGTGTATGACTG
TGGCTCTCACTCGCTCTCAGACTAAGACCCCAACCCCAATAGGGGAGGGCAGAGGGAAGCG
ATACATCCTTCCCCACCGCAGGCACCCCGGGGCTGGAGGGGCGTGTACCAAAATCCCGCG
CCATCAGCCTGGATGGGCATAAGTAGATAAATAACTGTGAGCTCGCAACAACCGAAAGGGCT
GACCCCTTACTTAGTCTCCCTCTTGAACAAGAGCAGACTGTGGAGAGCTGGGAGAGCGCA
GCCAGCTCGCTCTTTGCTGAGAGCCCTTTTGACAGAAAGCCAGCAGCACCCTGCTGGAAG
AACTGACAGTGCCCTCGCCCTCGGCCCGGGGCTGTGGGGTTGGATGCCCAGGTTCTATAC
ATATACATATATACACATCTATATAGAGAGATAGATATCTATTTTCCCTGTGGATTAG
CCCCGTGATGCTCCTGTTGGCTACGCAGGATGGGCAGTTGCACGAAGGCATGAATGTAT
TGTAATAAGTAACCTTGTACTTCTGAC

FIGURE 34

MLLWILLLETSLCFAAGNVTGDVCKEKICSCNEIEGDLHVDCEKKGFTSLQRFTAPTSQFYH
LFLHGNSLTRLPNEFANFYNAVSLHMENNGLHEIVPGAFLGLQLVKRLHINNKKISFRKQ
TFLGLDDLEYLQADFNLRRDIDPGAQDLNKLVLILNDNLISTLPANVFQYVPITHDLRG
NRLKTLPLYEEVLEQIPGIAETILLEDNPDWCTCDLLSLKLEWLENIPKNALIGRVVCEAPTRLQ
GKDLNETTEQDLCPLKNRVDSSLPAPPAQEETFAPGPLPTPFKTNQGEDHATPGSAPNGGTK
IPGNWQIKIRPTAAIATGSSRNKPLANSPLCPGGCSCDHIPGSGLKMNCCNNRNVSSLADLKP
KLSNVQELFLRDNKIHSIRKSHFVDYKNLILLDLGNNNIATVENNTFKNLLDLRWLYMDSNY
LDTLRSREKFPAGLQNLLEYLNVBYNAIQILIPGTFNAMPKLRILILNNNLLRSLPVDVFAGVSL
SKLSLHNMYFMYLPVAGVLDQLTSIIQIDLHGPNWECSCCTIVPFKQWAERLGSEVLMSDLKC
ETPVNFFRKDFMLLSNDEICPQLYARISPTLTSHSKNSTGLAETGTHSNSYLDTSRVSISVL
VPGLLLVPVTSAPTIVVGLVFIILNRKRKRKRDRANDSSASEINSLQTVCDSSYWHNGFPYNADG
AHRVYDCGSHSLSD

Signal sequence:

amino acids 1-15

Transmembrane domain:

amino acids 618-638

N-glycosylation site.

amino acids 18-22, 253-257, 363-367, 416-420, 595-599, 655-659

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 122-126, 646-650

Casein kinase II phosphorylation site.

amino acids 30-34, 180-184, 222-226, 256-260, 366-370, 573-577, 608-612, 657-661, 666-670, 693-697

N-myristoylation site.

amino acids 17-23, 67-73, 100-106, 302-308, 328-334, 343-349, 354-360, 465-471, 493-499, 598-604, 603-609

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 337-348

FIGURE 35

AGTCGACTGCGTCCCTGTACCCGGCGCCAGCTGTGTTCTGTACCCAGATAAACTCAGGGC
TGCACCGGGCCTGGCAGCGCTCCGCACACATTCTCTGTGCGGGCTAAGGGAAACTGTTGGC
CGTGGGCCCGCGGGGGATTCTTGGCAGTTGGGGGGTCCGTGCGGAGCGAGGGCGGAGGGG
AAGGGAGGGGGAACCGGTTGGGGAAGCCAGCTGTAGAGGGCGGTGACCGCGCTCCAGACAC
AGCTCTGCGTCTCGAGCGGGACAGATCCAAGTTGGGAGCAGCTCTGCGTGGGGGGCTCAG
AGAATGAGGCCCGCGTTTCGCCCTGTGCTCTCTGGCAGGCGCTTGGCCCGGGCCGGGGCGG
CGGCGAACACCCCACTGCGCAGCGTGTGGCTGCTCGGCCCTGGGGGGCTGTACAGCCTGC
ACCACGCTACCATGAAGCGGCAGGCGGCCGAGGAGGCTGCATCTCGCAGGTGGGGCGCTC
AGCACCGTGCCTGCGGGCGCCGAGCTGCGCGCTGTGCTCGCGCTCTTGGGGCAGGCCAGG
GCCCGGAGGGGGCTCCAAAGACCTGCTGTTCTGGGTGCGCACTGGAGCGCAGGCGTTCCCACT
GCACCTGGAGAACGAGCCTTTGCGGGGTTTCTCTGGCTGTCTCCGACCCCGCGCGTCTC
GAAAGCGACACGCTGCAGTGGGTGGAGAGCCCCAACGCTCTGACCCGCGCGGAGATGCGC
GGTACTCCAGGCCACCGTGGGGTCGAGCCCGCAGGCTGGAAGGAGATGCGATGCCACCTGC
GCGCAACGGGTACCTGTGCAAGTACCAGTTTGAGGTCTTGTGCTCTGCGCCGCGCCCGGG
GCCGCTCTAACTTGAGCTATCGCGCGCCCTTCCAGCTGCACAGCGCGCTCTGGACTTCAG
TCCACCTGGGACCGAGGTGAGTGCCTCTGCGGGGACAGCTCCCGATCTCAGTTACTTTGCA
TCGCGGACGAAATCGGCGCTCGTGGGACAAACTCTCGGGCGATGTGTTGCTCCCTGCCCC
GGGAGGTACCTCCGTGCTGGCAATGCGCAGAGCTCCCTAACTCCCTAGACGACTTGGGAGG
CTTTGCTGCGAATGTGCTACGGGCTTCGAGCTGGGGAAGGACGCGCTCTTGTGTGACCA
GTGGGGAAGGACAGCCGACCTTTGGGGGACCGGGGTGCCACCAGGCGCCCGCGGCCACT
GCAACAGCCCGTGTCGCGCAGAGAACATGGCCAATCAGGTCGACGAGAAGCTGGGAGAGAC
ACCACTTGTCCCTGAACAAGACAATTCAGTAACATCTATTCCTGAGATTCTCGATGGGGAT
CACAGAGCAGATGTCTACCCCTCAAATGTCCCTCAAGCCGAGTCAAAGGCCACTATCAC
CCATCAGGGAGCGTGATTTCGAAGTTAATTCTACGACTTCCCTGCGCACTCTCAGGCTTT
CGACTCTCTCTGTGCGTGGTCTTCATATTTGTGAGCACAGCAGTAGTAGTGTGGTGATCT
TGACCATGACAGTACTGGGGCTTGTCAAGCTCTGCTTTCACGAAAGCCCTCTTCCAGCCA
AGGAAGGAGTCTATGGGCCCGCGGGCTGGAGAGTGATCCTGAGCCGCTGCTTTGGGCTC
CAGTTCTGCACATTGCACAAACAATGGGGTGAAAGTCGGGGACTGTGATCTGCGGCACAGAG
CAGAGGTTGCGCTTGTGGCGGAGTCCCTCTTGGCTCTAGTGATGCAATAGGGAACAGGGGA
CATGGGCACTCTGTGAACAGTTTTTCACTTTTGATGAACCGGGGAACCAAGAGGAACCTTAC
TTGTGTAACCTGACATTTCTGCAGAATCCCCCTTCCTCAAATTCCTTTACTCCACTGAG
GAGCTAAATCAGAACTGCACACTCCTTCCCTGATGATAGAGGAAGTGGAAAGTGCCTTTAGGA
TGGTGATACTGGGGACCGGGTAGTGCTGGGGAGAGATATTTTCTTATGTTTATTCGAGAA
TTTGGAGAAGTGATTGAACCTTTTCAAGACATTGGAAACAAATAGAACACAATATAATTTACA
TTAAAAATAATTTTCAACCAATGAAAGGAAATGTTCTATGTTGTTTACGGCTAGGAGTAT
ATTGGTTCGAAATCCAGGGAAAAAATAAAAAATAAAAAATTAAGGATTGTTGAT

FIGURE 36

MRPAFALCLLWQALWPGPGGGEHPTADRAGCSASGACYSLHHATMKRQAAEEACILRGGALS
TVRAGAE LRAVLALLRAGPGPGGSKDLLFWVALERRRRSHCTLENEPLRGFSWLSSDPGGLE
SDTLQWVEEPQRSCTARRCAVLQATGGVEPAGWKEMRCHLRANGYLCKYQFEVLCPAPRPGA
ASNL SYRAPFQLHSAALDFSPPGTEVSALCRGQLPISVTCIADEIGARWDLKSGDVLCPCPG
RYLRAGKCAELPNCLLDDLGGFACECATGFELGKDGRSCVTSGBEQPTLGGTGVPTRRPPATA
TSPVPQRTWPIRVDEKLGETPLVPEQDNSVTSIPEIPRWGSQSTMSTLQMSLQAESKATITP
SGSVISKFNSTTSSATPQAFDSSSAVVFI FVSTAVVVLVILTMTVLGLVKLCFHESPSSQPR
KESMGPPGLESDPEPAALGSSSAHCTNNGVKVGDCDLRDRAGALLAESPLGSSDA

Signal sequence:

amino acids 1-16

Transmembrane domain:

amino acids 399-418

N-glycosylation site.

amino acids 189-193, 381-385

Glycosaminoglycan attachment site.

amino acids 289-293

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 98-102, 434-438

Casein kinase II phosphorylation site.

amino acids 275-279, 288-292, 342-346, 445-449

N-myristoylation site.

amino acids 30-36, 35-41, 58-64, 59-65, 121-127, 151-157,
185-191, 209-215, 267-273, 350-356, 374-380, 453-459, 463-469,
477-483

Aspartic acid and asparagine hydroxylation site.

amino acids 262-274

FIGURE 37

CGGACGCGTGGGATT CAGCAGTGGCCTGTGGCTGCCAGAGCAGCTCCTCAGGGGAAACTAAG
CGTCAGT CAGACGGCACCATAATCGCCTTTAAAGTGCCTCCGCCCTGCCGCCGCCGCTATC
CCCCGGCTACCTGGGCCGCCCGCGCGGTGCGCGCTGAGAGGGAGCGCGCGGCAGCCGA
GCGCCGCTGTGAGCCAGCGCTGTGCCAGTGTGAGCGCGGTGTGAGCGCGGTGGGTGCGGA
GGGCGTGTGTGCCGCCGCGCGCGCTGGGGTGCAAACCCCGAGCGTCTACGCTGCC**ATGA**
GGGGCGGAACGCCCTGGGCCCCACTCTGCCCTGCTGTGGCTGCCGCCACCCAGCTCTCGCG
CAGCAGTCCCCAGAGAGACTGTTTTACATGTGGTGGCATTCTTACTGGAGAGTCTGGATT
TATTGGCAGTGAAGGTTTTCTGGAGTGTACCCTCCAAATAGCAATGTACTTGGAAATCA
CAGTTCCCGAAGGAAAGTAGTCGTTCTCAATTTCCGATT CATAGACCTCGAGAGTGACAAC
CTGTGCCGTATGACTTTGTGGATGTGTACAATGGCCATGCCAATGCCAGCGCATTTGCCG
CTTCTGTGGCCTTTCCGGCCTGGAGCCCTTGTGTCCAGTGGCAACAAGATGATGGTGCAGA
TGATTTCTGATGCCAACACAGCTGGCAATGGCTTCATGGCCATGTTCTCCGCTGCTGAACCA
AACGAAAGAGGGGATCAGTATTGTGGAGGACTCCTTGACAGACCTTCCGGCTCTTTTAAAC
CCCCAAGTGGCCAGACCGGATTACCTTGACAGGAGTCACTTGTGTGTGGCATTGTAGCCC
CAAAGAATCAGCTTATAGAAATTAAGATTGAGAAGTTTGATGTGGAGCGAGATACTACTGC
CGATATGATTATGTGGCTGTGTTAATGGCGGGGAAGTCAACGATGTGAGAAGAATTGGAAA
GTATTGTGGTGATAGTCCACCTGCGCCAATTGTGTCTGAGAGAAATGAACCTTCTTATTAGT
TTTTATCAGACTTAAGTTTAACTGACAGATGGGTTTATTGGTCACTACATATTCAGGCCAAAA
AAACTGCCTACAACCTACAGAACAGCCTGTCAACCAACATTCCCTGTAAACCAAGGTTTAAA
ACCCACCGTGGCCTTGTGTCAACAAAAGTGTAGACGGACGGGACTCTGGAGGGCAATTATT
GTTCAAGTGACTTTGTATTAGCCGGCACTGTTATCAACCATCACTCGCGATGGGAGTTTG
CAGGCCACAGTCTCGATCATCAACATCTACAAAGAGGGAAATTGGCGATTACAGCAGGGGG
CAAGAACATGAGTGCCAGGCTGACTGTCGTCTGCAAGCAGTGCCCTCTCCTCAGAAGAGGTC
TAAATTACATTATTATGGGCCAAGTAGGTGAAGATGGGCGAGGCAAAATCATGCCAAACAGC
TTTATCATGATGTTCAAGACCAAGAATCAGAAGCTCCTGGATGCCTTAAAAAATAAGCAATG
TTAACAGTGAACTGTGCCATTTAAGCTGTATTCTGCCATTGCCTTTGAAAGATCTATGTTCT
TCTCAGTAGAAAAAAAATACTTTATAAAATTACATATTCTGAAAGAGGATTCGAAAGATGG
GACTGGTTGACTCTTACATGATGGAGGTATGAGGCCTCCGAGATAGCTGAGGGGAAGTTCTT
TGCTGTCTGT CAGAGAGCAGCTATCTGATTGGAAACCTGCCGACTTAGTGCGGTGATAGGA
AGCTAAAAGTGTCAAGCGTTGACAGCTTGGAAAGCGTTTATTATATACATCTCTGTAAAAGGAT
ATTTTGAATTGAGTTGTGTGAAGATGTCAAAAAAGATTTTGAAGTGCAATATTTATAGT
GTTATTTGTTTTACGCTTCAAGCCTTTGCCCTGAGGTGTTACAATCTTGCTCTGCGTTTTCTA
AATCAATGCTTAATAAAATATTTTAAAGGAAAAAAAAAAAAA

FIGURE 38

MRGANAWAPLCLLLAATQLSRQQSPERPVFTCGGILTGESGFIGSEGFPGVYPPNSKCTWK
ITVPEGKVVVLNFRFIDLESNDLCRYDFVDVYNHANGQRIGRFCGTFRPGALVSSGNKMMV
QMISDANTAGNGFMAMFSAAEPNERGDQYCGLLDRPSSGSKTPNWPDRDYPAGVTCVWHIV
APKNQLIELKFEKFDVERDNYCRYDYVAVFNGGEVNDARRIGKYCGDSFPAPIVSERNELLI
QFLSDLSLTADGFIGHYIFRPKKLPTTTEQPVTTTTFPVTTGLKPTVALCQCKRRTGTLEGN
YCSDFLVLAGTVITTITRDGSLHATVSIINIYKEGNLAIQQAGKNMSARLTVVCKQCPLLR
GLNYIIMGQVGEDGRGKIMPNSFIMMFKTKNQKLLDALKNKQC

Signal sequence:

amino acids 1-23

N-glycosylation site.

amino acids 355-359

Casein kinase II phosphorylation site.

amino acids 64-68, 142-146, 274-278

Tyrosine kinase phosphorylation site.

amino acids 199-208

N-myristoylation site.

amino acids 34-40, 35-41, 100-106, 113-119, 218-224, 289-295,
305-311, 309-315, 320-326, 330-336

Cell attachment sequence.

amino acids 149-152

FIGURE 39

CGGACGCGTGGGCGGACGCGTGGGCGGCCACGCGCCCCGCGGCTGGGGCGGTTCGCTTCTT
CCTTCTCCGTGGCCATACGAGGGTCCCCAGCCTGGGTAAAGATGGCCCCATGGCCCCGAAGG
GCCTAGTCCCAGCTGTGCTCTGGGGCCTCAGCCTCTTCTCAACCTCCCAGGACCTATCTGG
CTCCAGCCCTCTCCACCTCCCAGTCTTCTCCCCGCTCAGCCCCATCCGTGTACATCTG
CCGGGACTGGTTGACAGCTTTAAACAAGGGCCTGGAGAGAACCATCCGGGACAACCTTTGGAG
GTGGAACACATGCCTGGGAGGAAGAGAATTTGTCCAATACAAAGACAGTGAGACCCGCTG
GTAGAGGTGCTGGAGGGTGTGTGTCAGCAAGTCAGACTTCGAGTGCCACCGCCTGCTGGAGCT
GAGTGAGGAGCTGGTGGAGAGCTGGTGGTTTACAAGCAGCAGGAGGCCCGGACCTCTTCC
AGTGGCTGTGCTCAGATTCCTGTAAGCTCTGCTGCCCGCAGGCACTTCGGGCCCTCCTGC
CTTCCCTGTCTGGGGGAACAGAGAGGCCCTGCGGTGGCTACGGGCAGTGTAAGGAGAAGG
GACACGAGGGGGCAGCGGCCACTGTGACTGCCAAGCGGCTACGGGGGTGAGGCCCTGTGGCC
AGTGTGGCCTTGGCTACTTTGAGGCAGAACGCAACGCCAGCCATCTGGTATGTTTCGGCTTGT
TTTGGCCCCCTGTGCCGATGCTCAGGACCTGAGGAATCAAATCTGTTTGCAATGCAAGAAGGG
CTGGGCCCTGCATCACCTCAAGTGTGTAGACATTGATGAGTGTGGCAAGAGGGAGCCAACT
GTGGAGCTGACCAATTCTGCGTGAACACTGAGGGCTCCTATGAGTGCCGAGACTGTGCCAAG
GCCTGCCTAGGCTGCATGGGGGCAGGGCCAGGTGCTGTAAGAAGTGTAGCCCTGGCTATCA
GCAGGTGGGCTCCAAGTGTCTCGATGTGGATGAGTGTGAGACAGAGGTGTGTCGGGAGAGA
ACAAGCAGTGTGAAAAACCCAGGGGCGGTTATCGCTGCATCTGTGCCAGGGCTACAAGCAG
ATGGAAGGCATCTGTGTGAAGGAGCAGATCCAGAGTCAGCAGGCTTCTTCTCAGAGATGAC
AGAAGACGAGTTGGTGGTGTGCAGCAGATGTTCTTTGGCATCATCATCTGTGCACTGGCCA
CGCTGGCTGCTAAGGGCGACTTGGTGTTCACCGCCATCTTCATTGGGGCTGTGGCGGCCATG
ACTGGCTACTGGTTGTGTCAGAGCGCAGTGACCGTGTGCTGGAGGGCTTCATCAAGGGCAGATA
ATCGCGGCCACCACTGTAGGACCTCCTCCACCCACGCTGCCCCAGAGCTTGGGCTGCC
TCCTGCTGGACACTCAGGACAGCTTGGTTTATTTTGTAGAGTGGGGTAAGCACCCCTACCTG
CCTTACAGAGCAGCCAGGTACCCAGGCCCGGGCAGACAAGGCCCTGGGGTAAAAAGTAGC
CCTGAAGGTGGATACCATGAGCTTTCACCTGGCGGGGACTGGCAGGCTTCACAATGTGTGA
ATTTCAAAGTTTTTCTTAATGGTGGCTGCTAGAGCTTTGGCCCTGCTTAGGATTAGGTG
GTCTCTCACAGGGGTGGGGCCATCACAGCTCCCTCCTGCCAGTGCATGTGTCAGTTCCTGT
TCTGTGTTCCACCACATCCCACCCCATTGCCACTTATTATTATCTCAGGAATAAAGA
AAGGTCTGGAAAGTTAAAAAAAAAAAAAAAAAAAAAAAAA

FIGURE 40

MAPWPPKGLVPAVLWGLSLFLNLPGPIWLQPSPPPQSSPPPQPHPCHTCRGLVDSFNKGLER
TIRDNFGGGNTAWEEENLSKYKDSETRLVEVLEGVCSKSDFECHRLELSEELVESWWFHKQ
QEAPDLFWLCSDSLKCCPAGTFGPSCLPCPGGTERPCGGYGQCEGEGTRGGSGHCDQAG
YGGACGQCGLGYFEARNASHLVCSACFGPCARCSGPEESNCLQCKKGWALHHLKCVDIDE
CGTEGANCADQFCVNTESGYECRDCAKACLGCMGAGPGRCKKCSPGYQQVGSKCLDVDECE
TEVCPGENKQCENTEGGYRCICAEGYKQMEGICVKEQIPESAGFFSEMTEDELVVLLQQMFFG
IIICALATLAAKGDLVFTAIFIGAVAAMTGWLSERSDRVLEGFIKGR

Signal sequence:

amino acids 1-29

Transmembrane domain:

amino acids 372-395

N-glycosylation site.

amino acids 79-83, 205-209

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 290-294

Casein kinase II phosphorylation site.

amino acids 63-67, 73-77, 99-103, 101-105, 222-226, 359-263

N-myristoylation site.

amino acids 8-14, 51-57, 59-65, 69-75, 70-76, 167-173, 173-179,
177-183, 188-194, 250-256, 253-259, 267-273, 280-286, 283-289,
326-332, 372-378, 395-401

Aspartic acid and asparagine hydroxylation site.

amino acids 321-333

EGF-like domain cysteine pattern signature.

amino acids 181-193

FIGURE 41

TGAGACCCTCCTGCAGCCTTCTCAAGGGACAGCCCCACTCTGCCTCTTGCTCCTCCAGGGCA
GCACCATCCAGCCCCCTGTGGCTCTGCTGGGCACTCTGGGTGTTGCCCTGGCCAGCCCCGGG
GCCGCCCTGACCGGGGAGCAGCTCCTGGGCAGCCTGCTGCGGCAGCTGCAGCTCAAAGAGGT
GCCACCCCTGGACAGGGCCGACATGGAGGAGCTGGTCATCCCCACCCACGTGAGGGCCAGT
ACGTGGCCCTGCTGCAGCGCAGCCACGGGGACCGCTCCCGCGAAAGAGGTTAGCCAGAGC
TTCCGAGAGGTGGCCGGCAGGTTCTTGGCGTTGGAGGCCAGCACACACCTGCTGGTGTTCGG
CATGGAGCAGCGGCTGCCGCCCAACAGCGAGCTGGTGCAGGCCGTGCTGCGGCTCTTCCAGG
AGCCGGTCCCCAAGGCCGCGCTGCACAGGCACGGGCGGCTGTCCCGCGCAGCGCCCGGGCC
CGGGTGACCGCTCAGATGGCTGCGCGTCCGCGACGACGGCTCCAACCGCACCTCCCTCATCGA
CTCCAGGCTGGTGTCCGTCCACGAGAGCGGCTGGAAGGCCCTTCGACGTGACCGAGGCCGTGA
ACTTCTGGCAGCAGCTGAGCCGGCCCCGGCAGCCGCTGCTGTACAGGTGTCGGTGCAGAGG
GAGCATCTGGGCCCGCTGGCGTCCGGCGCCACAAGCTGGTCCGCTTTGGCTCGCAGGGGGC
GCCAGCCGGGCTTGGGGAGCCCCAGCTGGAGCTGCACACCTGGACCTTGGGGACTATGGAG
CTCAGGGCGACTGTGACCTGAAGCACCAATGACCGAGGGCACCCGCTGCTGCCGCCAGGAG
ATGTACATTGACCTGCAGGGGATGAAGTGGGCCGAGAACTGGTGCTGGAGCCCCGGGCTT
CCTGGCTTATGAGTGTGTGGGCACCTGCCGGCAGCCCCGGAGGCCCTGGCCTTCAAGTGGC
CGTTTCTGGGGCCTCGACAGTGCATCGCCTCGGAGACTGACTCGTGCCCATGATCGTCAGC
ATCAAGGAGGGAGGCAGGACCAGGCCCCAGGTGGTCAGCCTGCCCAACATGAGGGTGCAGAA
GTGCAGCTGTGCCTCGGATGGTGCCTCGTGCCAAGGAGGCTCCAGCCATAGCGCCTAGTG
TAGCCATCGAGGGACTTGACTTGTGTGTTTCTGAAGTGTCGAGGGTACCAGGAGAGCTG
CGGATGACTGAACTGCTGATGGACAAATGCTCTGTGCTCTCTAGTGAGCCCTGAATTGCTT
CCTCTGACAAGTTACCTCACCTAATTTTGTCTTCTCAGGAATGAGAATCTTTGGCCACTGGA
GAGCCCTTGCTCAGTTTTCTATTCTTATTATTCACTGCACTATATTCTAAGCACTTACAT
GTGGAGATACTGTAACCTGAGGGCAGAAAGCCANTGTGTCAATTGTTTACTTGTCTGTGAC
TGGATCTGGGCTAAAGTCTCCACCACCACTCTGGACCTAAGACCTGGGGTTAAGTGTGGGT
TGTGCATCCCCAATCCAGATAATAAGACTTTGTAAAACATGAATAAAACACATTTTATTCT
AAAA

FIGURE 42

MQPLWLCWALWVLPLASPGAALTGEQLLGSLLRQLQLKEVPTLDRADMEELVIPTHVRAQYV
ALLQRSHGDRSRGKRFSQSFPREVAGRFLALEASTHLLVFGMEQRLPPNSELVQAVLRLFQEP
VPKAALHRHGRLSPRSARARVTVEWLRVRDDGSNRTSLIDSRLVSVHESGWKAFDVTEAVNF
WQQLSRPRQPLLLQVSVQREHLGFLASGAHKLVRFASQGAPAGLGEPQLELHTLDLGDYGAQ
GDCDPEAFMTEGTRCCRQEMYIDLQGMKWAENWVLEPPGFLAYECVGTCTCRQPPEALAFKWWF
LGPRQCIASETDSLPMIVSIKEGGRTRPQVVSLPNMRVQKCSASDGALVPRRLQP

Signal sequence:

amino acids 1-18

N-glycosylation site.

amino acids 158-162

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 76-80

Casein kinase II phosphorylation site.

amino acids 68-72, 81-85, 161-165, 169-173, 319-323, 329-333

N-myristoylation site.

amino acids 19-25, 156-162, 225-231, 260-266, 274-280

Amidation site.

amino acids 74-78

TGF-beta family signature.

amino acids 282-298

FIGURE 43

GTCTGTTCCAGGAGTCTTCGGCGGCTGTTGTGTCAGTGGCCTGATCGCGAATGGGGACAAA
GGCGCAAGTCGAGAGGAAACTGTTGTGCCTCTTCATATTGGCGATCCTGTTGTGCTCCCTGG
CATTGGGCAGTGTTACAGTGCACCTCTCTGAACCTGAAGTCAGAATTCCTGAGAATAATCCT
GTGAAGTTGTCTGTGCCTACTCGGGCTTTTCTCTCCCGTGTGGAGTGAAGTTTGACCA
AGGAGACACCACCAGACTCGTTTGCTATAATAACAGATCACAGCTTCCTATGAGGACCGGG
TGACCTTCTTGCCAACCTGGTATCACCTTCAAGTCCGTGACACGGGAAGACA CTGGGACATAC
ACTTGATATGGTCTCTGAGGAAGCGCGCAACAGCTATGGGGAGGTCAAGGTCAAGCTCATCGT
GCTTGTGCCTCCATCCAAGCCTACAGTTAACATCCCCCTCCTCTGCCACCATTGGGAACCGGG
CAGTGTCTGACATGCTCAGAACAAGATGGTTCCCCACCTTCTGAATACACCTGGTTCAAAGAT
GGGATAGTGATGCCATACGAATCCCAAAGCACCCCGTGCCTTCAGCAACTCTTCCTATGTCTCT
GAATCCCAACAACAGGAGAGCTGGTCTTTGATCCCTGTGAGCCTCTGATACTGGAGAATACA
GCTGTGAGGCACGGAATGGGTATGGGACACCCATGACTTCAAATGCTGTGCGCATGGAAGCT
GTGGAGCGGAATGTGGGGGTCTCGTGGCAGCCGTCCTGTGAACCTGATTCTCCTGGGAAT
CTTGGTTTTTTGGCATCTGGTTTTGCCCTATAGCCGAGGCCACTTTGACAGAAACAAAGAAAGGGA
CTTCGAGTAAGAAGGTGATTACAGCCAGCCTAGTGCCCGAAGTGAAGGAGAATTCAAACAG
ACCTCGTCATTCTGGTGTGAGCCTGGTGGCTCACCGCCTATCATCTGCATTGTGCCTTACT
CAGGTGTACCGGACTCTGGCCCTGATGTCTGTAGTTTTACAGGATGCCTTATTGTCTTC
TACACCCACAGGGCCCCCTACTTCTCGGATGTGTTTTTAATAATGTGAGTATGTGCCCC
ATCCTCCTTCATGCCCTCCCTCCCTTCTCTACCCTGCTGAGTGGCCTGGAACCTGTTTTAAA
GTGTTTTATTCCCATTTCTTTGAGGGATCAGGAAGGAATCCTGGGTATGCCATTGACTTCCC
TTCTAAGTAGACAGCAAAAATGGCGGGGTGCGAGGAATCTGCACTCAACTGCCACCTGGC
TGGCAGGGATCTTTGAATAGGTATCTTGAGCTTGTTCTGGGCTCTTTCTTGTGTACTGAC
GACCAGGGCCAGCTGTTCTAGAGCGGAATTAGAGGCTAGAGCGGCTGAAATGGTTGTTTGG
TGATGACACTGGGGTCTTCCATCTCTGGGGCCCACTCTCTTCTGTCTTCCATGGGAAGTG
CCACTGGGATCCCTCTGCCCTGTCTCTCTGAATACAAGCTGACTGACATTGACTGTGTCTGT
GGAAATGGGAGCTCTTGTGTGGAGAGCATAGTAAATTTTCAGAGAACCTGAAGCCAAAAAG
GATTTAAAACCGCTGCTCTAAAGAAAAGAAAACCTGGAGGCTGGGCGCAGTGGCTCACGCCTG
TAATCCAGAGGCTGAGGCAGGCGGATCACCTGAGGTCGGGAGTTTGGGATCAGCTGACCTGACCA
ACATGGAGAAACCTACTGGAATAACAAAGTTAGCCAGGCATGGTGGTGCATGCCTGTAGTC
CCAGCTGCTCAGGAGCCTGGCAACAAGAGCAAAACTCCAGCTCAAAAAAAAAAAAAAAAAA

FIGURE 44

MGTKAQVERKLLCLFILAILLCSLALGSVTVHSSEPEVRIPENNPVKLS CAYSGFSSPRVEW
KFDQGDITTRLVCYNNKITASYEDRVTFLLPTGITFKSVTREDTGTYTCMVSEEGNSYGEVKV
KLIVLVPPSKPTVNIPISSATIGNRAVLTCS EQDGSPPSEYTWFKDGIVMPTNPKSTRAFSNS
SYVLNPTTGELVFDPLSASDTGEYSCEARNGYGTTPMTSNAVRMEAVERNVGIVAAVLVTLI
LLGILVFGIWFAYS RGHFDRTKKGTSSKKVIYSQPSARSEGEFKQTSSFLV

Signal sequence:

amino acids 1-27

Transmembrane domain:

amino acids 238-255

N-glycosylation site.

amino acids 185-189

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 270-274

Casein kinase II phosphorylation site.

amino acids 34-38, 82-86, 100-104, 118-122, 152-156, 154-158,
193-197, 203-207, 287-291

N-myristoylation site.

amino acids 105-111, 116-122, 158-164, 219-225, 237-243, 256-262

FIGURE 45

CAGCGCGTGGCCGGCGCCGCTGTGGGGACAGCATGAGCGCGGTTGGATGGCGCAGGTTGGA
GCGTGGCGAACAGGGGCTCTGGGCTGGCGCTGCTGCTGCTCGGCCTCGGACTAGGCCT
GGAGGCCGCCGAGCCCGCTTTCCACCCGACCTCTGCCAGGCCGAGGCCCCAGCTCAG
GCTCGTGCCACCCACCAAGTTCAGTGCCGCACCAAGTGGCTTATGCGTGCCCCCTCACCTGG
CGCTGCGACAGGGACTTGGACTGACGCGATGGCAGCGATGAGGAGGAGTGACAGGATTGAGCC
ATGTACCAGAAAAGGGCAATGCCACCGCCCCCTGGCCTCCCCTGCCCCCTGCACCGGCGTCA
GTGACTGCTCTGGGGGAAGTGAACAAGAACTGCGCAACTGCAGCCGCTGGCCTGCCTAGCA
GGCGAGCTCCGTTGCACGCTGAGCGATGACTGCATTCCACTCACGTGGCGCTGCGACGGCCA
CCCAGACTGTCCGACTCCAGCGACGAGCTCGGCTGTGGAACCAATGAGATCCTCCCGGAAG
GGGATGCCACAACCATGGGGCCCCCTGTGACCTGGAGAGTGTACCTCTCTCAGGAATGCC
ACAAACATGGGGCCCCCTGTGACCCTGGAGAGTGTCCCCTCTGTCGGGAATGCCACATCCTC
CTCTGCCGGAGACCAGTCTGGAAGCCCAACTGCCTATGGGGTTATTGCAGCTGCTGCGGTGC
TCAGTGCAAGCCTGGTACCGCCACCCCTCCTCCTTTGTCTGGCTCCGAGCCAGGAGCGC
CTCCGCCCACTGGGGTTACTGGTGGCCATGAAGGAGTCCCTGCTGCTGTGAGACAGAAGAC
CTCGCTGCCCTGAGGACAAGCACTTGCCACCACCGTCACTCAGCCCTGGGCGTAGCCGGACA
GGAGGAGAGCAGTGATGCGGATGGGTACCGGGCACACCAGCCCTCAGAGACCTGAGTTCTT
CTGGCCACGTGGAACCTCGAACCCGAGCTCCTGCAGAAGTGGCCCTGGAGATTGAGGGTCCC
TGGACACTCCCTATGGAGATCCGGGGAGCTAGGATGGGGAACTGCCACAGCCAGAACTGAG
GGCTGGCCCCAGGCAGCTCCAGGGGGTAGAACGGCCCTGTGCTTAAGACACTCCCTGCTG
CCCCGCTTGAGGGTGGCGATTAAAGTTGCTTC

FIGURE 46

MSGGWMAQVGAWRTGALGLALLLLGLGLGLEAAASPLSTPTSAQAAGPSSGSCPPTKFCR
TSGLCVPLTWRCRDLDCSDGSDEEECRIEPCTQKGQCPPPGLPCPCTGVSDCSGGTDKKL
RNC SRLACLAGE LRCTLSDDCIPLTWRC DGHPCDPSDELGCGTNEILPEGDATTMGPPVT
LESVTS LRNATMGPPVTLESVPSVGNATSSSAGDQSGSPTAYGVIAAAVLSASLVTATLL
LLSWLRAQERLRPLGLLVAMKESLLLSEQKTSLP

Signal sequence:

amino acids 1-30

Transmembrane domain:

amino acids 230-246

N-glycosylation site.

amino acids 126-130, 195-199, 213-217

Casein kinase II phosphorylation site.

amino acids 84-88, 140-144, 161-165, 218-222

N-myristoylation site.

amino acids 3-9, 10-16, 26-32, 30-36, 112-118, 166-172, 212-218,
224-230, 230-236, 263-269

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 44-55

Leucine zipper pattern.

amino acids 17-39

FIGURE 47

CCCACGCGTCCGGTCTCGCTCGCTCGCGCAGCGGCGGCAGCAGAGGTCGCGCACAGATGCGG
GTTAGACTGGCGGGGGAGGAGGCGGAGGAGGAAGGAAGCTGCATGCATGAGACCCACAGA
CTCTTGCAAGCTGGATGCCCTCTGTGGATGAAAGATGTATCATGGAATGAACCCGAGCAATG
GAGATGGATTCTTAGAGCAGCAGCAGCAGCAGCAACCTCAGTCCCCCAGAGACTCTTG
GCCGTGATCCTGTGGTTTCAGCTGGCGCTGTGCTTCGGCCCTGCACAGCTCACGGGCGGGTT
CGATGACCTTCAAGTGTGTGCTGACCCCGGCATTCCCGAGAATGGCTTCAGGACCCACAGCG
GAGGGGTTTTCTTTGAAGGCTCTGTAGCCCGATTTCAC TGCCAAAGACGGATTCAAGCTGAAG
GGCGCTACAAAGAGACTGTGTTTGAAGCATTTTAATGGAACCCTAGGCTGGATCCCAAGTGA
TAATTCATCTGTGTGCAAGAAGATTGCCGTATCCCTCAAATCGAAGATGCTGAGATTCATA
ACAAGACATATAGACATGGAGAGAAGCTAATCATCACTTGTCATGAAGGATTCAAGATCCGG
TACCCCGACCTACACAATATGGTTTCATTATGTGCGGATGATGGAACGTGGAATAATCTGCC
CATCTGTCAAGGCTGCCGTGAGACCTCTAGCCTCTTCTAATGGCTATGTAAACATCTCTGAGC
TCCAGACCTCCTTCCCGGTGGGACTGTGATCTCCTATCGCTGCTTTCCCGGATTTAACCTT
GATGGGTCTGCGTATCTTGAGTGCTTACAAAACCTTATCTGGTCGTCCAGCCACCCCGGTG
CCTTGCTCTGGAAGCCCAAGTCTGTCCACTACCTCCAATGGTGAGTCACGGAGATTTCTGCT
GCCACCCGCGGCTTGTGAGCGCTACAACCACGGAACGTGGTGAGATTTTACTGCGATCCT
GGCTACAGCCTCACCAGCGACTACAAGTACATCACCTGCCAGTATGGAGAGTGGTTTCCTTC
TTATCAAGTCTACTGCATCAAATCAGAGCAAACGTGGCCGACACCCATGAGACCTCCTGA
CCACGTGGAAGATTGTGGCGTTCACGGCAACCAGTGTGCTGCTGGTGTGCTGCTCGTCATC
CTGGCCAGGATGTTCCAGACCAAGTTCAAGGCCACTTTCCCCCAGGGGCTCCCCGAG
TTCCAGAGTGACCTTGACTTTGTGGTGGTAGACGGCGTGCCCGTCATGCTCCCGTCCTATG
ACGAAGCTGTGAGTGGCGCTTGAGTGCTTAGGCCCGGGTACATGGCCTCTGTGGGCCAG
GGCTGCCCTTACCCGTGGACGACAGAGCCCCCAGCATACCCCGGCTCAGGGGACACGGA
CACAGGCCAGGGGAGTCAGAAACCTGTGACAGCGTCTCAGGCTCTTCTGAGCTGCTCCAAA
GTCTGTATTACCTCCAGGTGCCAAGAGAGCACCACCTGCTTCGGACAACCTTGACATA
ATTGCCAGCACGGCAGAGGAGTGGCATCCACCAGCCAGGCATCCATCATGCCCACTGGGT
GTGTTCTTAAGAAACTGATTGATTGATTAATAAAATTTCCAAAGTGCTGAAGTGTCTCTCAA
ATACATGTTGATCTGTGGAGTTGATTCTTTCTTCTCTTGGTTTTAGACAAATGTAAACAA
AGCTCTGATCCTTAAATTGCTATGCTGATAGAGTGGTGAGGCTGGAAGCTTGATCAAGTC
CTGTTTCTTCTTGACACAGACTGATTAAAAATTAAAGNAAAAA

FIGURE 48

MYHGMNPSNGDGFLEQQQQQQPQSPQRLLAVILWFQLALCFGPAQLTGGFDDLQVCADPGI
PENGFRTPSGGVFFEGSVARFHCQDGFKLKGATKRLCLKHFNGTLGWIPSDNSICVQEDCRI
PQIEDAEIHNKTYRHGEKLIITCHEGFKIRYPDLHNMVSLCRDDGTWNNLPICQGCLRPLAS
SNGYVNISELQTSFPVGTVISYRCFPGFKLDGSAYLECLQNLIWSSSPRCLALEAQVCPLP
PMVSHGDFVCHPRPCERYNHGTVVEFYCDPGYSLTSDYKYITCQYGEWFPSYQVYCIKSEQT
WPSTHETLLTTWKIVAFTATSVLLVLLLVILARMFQTKFKAHFEPGPRSSSSDPDFVVVD
GVPVMLPSYDEAVSGGLSALGPGYMASVGGCPLPVDDQSPPAYPGSGDTDTGPGSESETCDS
VSGSSELLQSLYSPRCQESTHPASDNPDIIASTAEVASTSPGIHHAHWLFLRN

Signal sequence:

amino acids 1-41

Transmembrane domain:

amino acids 325-344

N-glycosylation site.

amino acids 104-108, 134-138, 192-196

Casein kinase II phosphorylation site.

amino acids 8-12, 146-150, 252-256, 270-274, 313-317, 362-366,
364-368, 380-384, 467-471, 468-472

N-myristoylation site.

amino acids 4-10, 61-67, 169-175, 203-209, 387-393, 418-424,
478-484

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 394-405

FIGURE 49

CCCACGCGTCCGCTCCGCGCCCTCCCCCGCCTCCCGTGCGGTCCGTCCGGTGGCCTAGAGA
TGCTGCTGCCGCGGTTGCAGTTGTGCGGCACGCCTCTGCCCGCAGCCCGCTCCACGCGCGT
AGCGCCCGAGTGTGCGGGGGCGCACCCGAGTCGGGCCATGAGGCCGGGAACCGCGCTACAGG
CCGTGCTGCTGGCCGTGCTGCTGGTGGGGCTGCGGGCCGCGACGGTTCGCTGCTGAGTGCC
TCGGATTGGACCTCAGAGGAGGGCAGCCAGTCTGCCGGGAGGGACACAGAGGCCCTTGTTA
TAAAGTCATTTACTTCCATGATACTTCTCGAAGACTGAACCTTTGAGGAAGCCAAAGAAGCCT
GCAGGAGGGATGGAGGCCAGCTAGTCAGCATCGAGTCTGAAGATGAACAGAACTGATAGAA
AAGTTCATTGAAAACCTCTTGCCATCTGATGGTGACTTCTGGATTGGGCTCAGGAGGCGTGA
GGAGAAACAAAGCAATAGCACAGCCTGCCAGGACCTTTATGCTTGGACTGATGGCAGCATAT
CACAAATTTAGGAACTGGTATGTGGATGAGCCGTCTGCGGCAGCGAGGTCTGCGTGGTCATG
TACCATCAGCCATCGGCACCCGCTGGCATCGGAGGCCCTACATGTTCCAGTGGAATGATGA
CCGTGTGCAACATGAAGAACAAATTCATTGCAATATCTGATGAGAAACAGCAGTTCTCTT
CTAGAGAAGCTGAAGGTGAGGAAACAGAGCTGACAAACCTGTACTTCCAGAAGAACACAG
GAAGAAGATGCCAAAAAACATTTAAAGAAAGTAGAGAAGCTGCCTTGAATCTGGCCTACAT
CCTAATCCCCAGCATTCCCCCTTCTCCTCCTCTTGTGGTCACCACAGTTGTATGTTGGGTTT
GGATCTGTAGAAAAAGAAAACGGGAGCAGCCAGACCTAGCACAAAGAAGCAACACACCATC
TGGCCCTCTCCTCACCAGGGAAACAGCCCGACCTAGAGGTCTACAATGTCATAAGAAAAACA
AAGCGAAGCTGACTTAGCTGAGACCCGGCCAGACCTGAAGAATATTTCAATCCGAGTGTGTT
CGGGAGAAGCCACTCCCGATGACATGTCTTGTGACTATGACAACATGGCTGTGAACCCATCA
GAAAGTGGGTTTGTGACTCTGGTGAGCGTGGAGAGTGGAATTTGTGACCAATGACATTTATGA
GTTCTCCCCAGACCAATGGGGAGGAGTAAGGAGTCTGGATGGGTGGAAAATGAAATATATG
GTTATTAGGACATATAAAAAAAGTAACTGAACTGACAACAAATGAAAAAGAAATGATAAGCAAAATC
CTCTATTTTCTATAAGGAAAAATACACAGAAGGTCTATGAACAAGCTTAGATCAGGTCCTGT
GGATGAGCATGTGGTCCCCACGACCTCCTGTTGGACCCCAACGTTTTGGCTGTATCCTTTAT
CCCAGCCAGTCATCCAGCTCGACCTTATGAGAAGGTACCTTGCCAGGTCTGGCAGATAGTA
GAGTCTCAATAAATGTCACTTGGTTGGTTGTATCTAACTTTTAAAGGACAGAGCTTTACCTG
GCAGTGATAAAGATGGGCTGTGGAGCTTGAAAAACCACTCTGTTTTCTTGCTCTATACAG
CAGCACATATTATCATACAGACAGAAAAATCCAGAACTTTTCAAAGCCCACATATGGTAGCACAG
GTTGGCCTGTGCATCGGCAATTCATATCTGTTTTTTCAAAGAATAAAATCAAATAAAGA
GCAGGAAAAA

FIGURE 50

MRPGTALQAVLLAVLLVGLRAATGRLLSASDLDLRGGQPVCRRGGTQRPCYKVIYFHDTSRRL
NFEEAKEACRRDGGQLVSI ESEDEQKLI EKFIENLLPSDGDWFIGLRRREEKQSNSTACQDL
YAWTDGSI SQFRNWIYVDEPSCGSEVCVVMYHQPSAPAGIGGPYMFQWNDDRCNMKNNFICKY
SDEKPAVPSREAEGEETELTTPVLPEETQEEDAKKTFKESREAAALNLAYILIPS I PLLLLL
VTTVVCVWVICRKRKREQPDSTKKQHTIWPSPHQGNSPDLEVYNVIRKQSEADLAETRPDL
KNISFRVCSGEATPDDMSCDYDNMAVNPSES GFVTLVSVESGFVTNDIYEFSPDQMGRSKES
GWVENEIYGY

Signal sequence:

amino acids 1-21

Transmembrane domain:

amino acids 235-254

N-glycosylation site.

amino acids 117-121, 312-316

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 296-300

Casein kinase II phosphorylation site.

amino acids 28-32, 30-34, 83-87, 100-104, 214-218, 222-226,
299-303, 306-310, 323-327

N-myristoylation site.

amino acids 18-24, 37-43, 76-82, 146-152

FIGURE 51

GGGGTCTCCCTCAGGGCCGGGAGGCACAGCGGTCCCTGCTTGCTGAAGGGCTGGATGTACGC
ATCCGAGGTTCCCGCGACTTGGGGGCGCCCGCTGAGCCCCGGCGCCCGAGAAGACTTGT
GTTTGCCCTCCTGCAGCCTCAACCCGAGGGGCAGCGAGGGCCTACCACCATGATCACTGGTGT
GTTCAGCATGCGCTTGTGGACCCAGTGGGCGTCTGACCTCGTGGCGTACTGCCTGCACC
AGCGGCGGGTGGCCCTGGCCGAGCTGCAGGAGGCCGATGGCCAGTGTCCGGTCGACCGCAGC
CTGCTGAAGTTGAAATGGTGCAGGTCGTGTTTCGACACGGGGCTCGGAGTCTCTCAAGCC
GCTCCCGCTGGAGGAGCAGGTAGAGTGGAACCCAGCTATTAGAGGTCCACCCCAAACCTC
AGTTTGATTACACAGTACCAATCTAGCTGGTGGTCCGAAACCATATTCTCCTTACGACTCT
CAATACCATGAGACCACCCCTGAAGGGGGGCATGTTTGCTGGGCAGCTGACCAAGTGGGCAT
GCAGCAAATGTTTGCCTTGGGAGAGAGACTGAGGAAGAACTATGTGGAAGACATTCCCTTTC
TTTCACCAACCTTCAACCCACAGGAGGTCTTTATTCGTTCCACTAACATTTTCGGAATCTG
GAGTCCACCCGTTGTTTGCTGGCTGGGCTTTTCCAGTGTCAGAAAGAAGGACCCATCATCAT
CCACACTGATGAAGCAGATTCAAGTCTTGATCCCAACTACCAAAGCTGCTGGAGCCCTGA
GGCAGAGAACCAGAGGCCGAGGCAGACTGCCTCTTTACAGCCAGGAATCTCAGAGGATTTG
AAAAAGGTGAAGGACAGGATGGGCATTGACAGTAGTGATAAAGTGGACTTCTTCATCCTCCT
GGACAACGTGGCTGCCGAGCAGGCACACAACCTCCCAAGCTGCCCATGCTGAAGAGATTTG
CACGGATGATCGAACAGAGAGCTGTGGACACATCCTTGACATACTGCCAAGGAAGACAGG
GAAAGTCTTCAGATGGCAGTAGGCCATTCTCCACATCTTAGAGAGCAACCTGCTGAAAGC
CATGGACTCTGCCACTGCCCCGACAAGATCAGAAAGCTGTATCTCTATGCGGCTCATGATG
TGACCTTCATACCGCTCTTAATGACCTGGGGATTTTGACCACAAATGGCCACCGTTTGCT
GTTGACCTGACCATGGAACCTTACCAGCACCTGGAATCTAAGGAGTGGTTTGTGCAGCTCTA
TTACCACGGGAAGGAGCAGGTGCCGAGAGGTTGCCCTGATGGGCTCTGCCCGCTGGACATGT
TCTTGAATGCCATGTGAGTTTATACCTTAAGCCAGAAAAATACCATGCACTCTGCTCTCAA
ACTCAGGTGATGGAAGTTGGAATGAAGAGTAACTGATTATATAAAGCAGGATGTGTTGATT
TTAAAATAAAGTGCCCTTTATACAATG

FIGURE 52

MITGVFSMRLWTPVGVLTSLAYCLHQRRVALAELQEADGQCPVDRSLLKLMVQVVFRHGAR
SPLKPLPLEEQVEWNPQLLEVPPQTQFDYTTVINLAGGPKPYSPYDSQYHETTLKGGMFAGQL
TKVGMQMQMFALGERLRKNYVEDIPFLSPTFNPQEVFIRSTNIFRNLESTRCLLAGLFCQCKE
GPIIIHTDEADSEVLYPNYQSCWSLRQRTGRRRQTASLQPGISEDLLKKVKDRMGIDSSDKVD
FFILLDNVAEQAHNLPSCPMLKKRFARMIEQRAVDTSLYILPKEDRESLQMAVGPPFLHILES
NLLKAMDSATAPDKIRKLYLYAAHDVTFIPLLMTLGIFDHKWPPFAVDLTMELYQHLESKEW
FVQLYYHGKEQVPRGCPDGLCPDLMFLNAMS VYTLSPKEYHALCSQTQVMEVGNEE

Signal sequence:

amino acids 1-23

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 218-222

Casein kinase II phosphorylation site.

amino acids 87-91, 104-108, 320-324

Tyrosine kinase phosphorylation site.

amino acids 280-288

N-myristoylation site.

amino acids 15-21, 117-123, 118-124, 179-185, 240-246, 387-393

Amidation site.

amino acids 216-220

Leucine zipper pattern.

amino acids 10-32

Histidine acid phosphatases phosphohistidine signature.

amino acids 50-65

FIGURE 53

CTCCTCTTAACATACTTGCAGCTAAAACTAAATATTGCTGCTTGGGGACCTCCTTCTAGCCT
TAAATTTACAGCTCATCACCTTCACCTGCCTTGGTCATGGCTCTGCTATTCTCCTTGATCCTT
GCCATTTGCACACAGACCTGGATTCTCTAGCGTCTCCATCTGGAGTGC GGCTGGTGGGGGGCCT
CCACCGCTGTGAAGGGCGGGTGGAGGTGGAACAGAAAGGCCAGTGGGGCACCGTGTGTGATG
ACGGCTGGGACATTAAGGACGTGGCTGTGTTGTGCCGGGAGCTGGGCTGTGGAGCTGCCAGC
GGAACCCCTAGTGGTATTTTGTATGAGCCACCAGCAGAAAAAGAGCAAAAGGTCTCATCCA
ATCAGTCAGTTGCACAGGAACAGAAAGATACATTGGGCTCAGTGTGAGCAAGAAGAAGTTTATG
ATTGTTTACATGATGAAGATGCTGGGGCATCGTGTGAGAAGCCAGAGAGCTCTTTCTCCCCA
GTCCCAGAGGGTGTGAGGCTGGCTGACGGCCCTGGGCATTGCAAGGGACGCGTGAAGTGAA
GCACCAGAACCAAGTGGTATACCGTGTGCCAGACAGGCTGGAGCCTCCGGGGCGCAAGGTGG
TGTGCCGGCAGCTGGGATGTGGGAGGGCTGTACTGACTCAAAAACGCTGCAACAAGCATGCC
TATGGCCGAAAAACCATCTGGCTGAGCCAGATGTCATGCTCAGGACGAGAAGCAACCTTCA
GGATTGCCCTTCTGGGCCTTGGGGGAAGAACACCTGCAACCATGATGAAGACACGTGGGTCG
AATGTGAAGATCCCTTTGACTTGAGACTAGTAGGAGGAGACAACCTCTGCTCTGGGCGACTG
GAGGTGCTGCACAAGGGCGTATGGGGCTCTGTCTGTGATGACAAGTGGGGAGAAAAGGAGGA
CCAGGTGGTATGCAAGCAACTGGGCTGTGGGAAGTCCCTCTCTCCCTCCTTCAGAGACCGGA
AATGCTATGGCCCTGGGGTGTGGCCGCATCTGGCTGGATAATGTTGCTGCTCAGGGGAGGAG
CAGTCCCTGGAGCAGTGCCAGCACAGATTTTGGGGGTTTCACGACTGCACCCACCAGGAAGA
TGTGGCTGTCTCTGCTCAGTGTAGGTGGGCATCATCTAATCTGTTGAGTGCCTGAATAGAA
GAAAAACACAGAAGAAGGGAGCATTTACTGTCTACATGACTGCATGGGATGAACACTGATCT
TCTTCTGCCCTTGGACTGGGACTTATACTTGGTGCCCTGATTCTCAGGCCCTTCAGAGTTGG
ATCAGAAGTTACAACATCAGGTCTAGTTCTCAGGCCATCAGACATAGTTTGGAACTACATCA
CCACCTTTTCCTATGTCTCCACATTGCACACAGCAGATTCAGGCCCTCCATAATTGTGTGTAT
CAACTACTTAAATACATTCTCACACACACACACACACACACACACACACACACATA
CACCATTGTCTCTGTTTCTCTGAAGAACTCTGACAAAATACAGATTTTGGTACTGAAAGAGA
TTCTAGAGGAACGGAATTTTAAAGGATAAAATTTCTGAATTGGTTATGGGGTTTCTGAAATTG
GCTCTATAATCTAATTAGATATAAAATCTGGTAACCTTTATTACAATAATAAGATAGCAC
TATGTGTTCAAA

FIGURE 54

MALLFSLILAICTRPGFLASPSGVRVLVGGLHRCGRVEVEQKGQWGTVCDDGWDIKDVAVLC
RELGCGAASGTPSGILYEPPAEKEQKVLIQSVSCTGTEDTLAQCEQEVEYDCSHDEDAGASC
ENPESFSFPVPEGVRLADGPGHCKGRVEVKHQNQWYTVQCQTGWSLRAAKVVCRLGCGRAVL
TQKRCNKHAYGRKPIWLSQMSCSGREATLQDCPSGPGWKNTCNHDEDTWVECEDPFDLRLVG
GDNLCSGRLEVLHKGVWGSVCCDDNWGEKEDQVVCKQLGCGKSLSPSFRDRKCYGPGVGRIWL
DNVRCSGEEQSLEQCQHRFWGFHDCTHQEDVAVICSV

Signal sequence:

amino acids 1-15

Casein kinase II phosphorylation site.

amino acids 47-51, 97-101, 115-119, 209-213, 214-218, 234-238,
267-271, 294-298, 316-320, 336-340

N-myristoylation site.

amino acids 29-35, 43-49, 66-72, 68-74, 72-78, 98-104, 137-143,
180-186, 263-269, 286-292

Amidation site.

amino acids 196-200

Speract receptor repeated domain signature.

amino acids 29-67, 249-287

FIGURE 55

ACTGCACTCGGTTCTATCGATTGAATCCCCGGGGATCCTCTAGAGATCCCTCGACCTCGAC
CCACGCGTCCGCGGACGCGTGGGCGGACGCGTGGGCCGGCTACCAGGAAGAGTCTGCCGAAG
GTGAAGGCCATGGACTTCATCACCTCCACAGCCATCCTGCCCTGCTGTTCGGCTGCCTGGG
CGTCTTCGGCTCTTCCGGCTGCTGCAGTGGGTGCGCGGGAAGGCCCTACCTGCGGAATGCTG
TGGTGGTGATCACAGGCGCCACCTCAGGGCTGGGCAAAGAATGTGCAAAAGTCTTCTATGCT
GCGGGTGCTAAACTGGTGCTCTGTGGCCGGAATGGTGGGGCCCTAGAAGAGCTCATCAGAGA
ACTTACCGCTTCTCATGCCACCAAGGTGCAGACACACAAGCCTTACTTGGTGACCTTCGACC
TCACAGACTCTGGGGCCATAGTTTGACGAGCAGCTGAGATCCTGCAGTGCTTTGGCTATGTC
GACATACTTGTCACAATGCTGGGATCAGCTACCGTGGTACCATCATGGACACCACAGTGA
TGTGGACAAGAGGGTCATGGAGACAAACTACTTTGGCCAGTTGCTCTAACGAAAGCACTCC
TGCCCTCCATGATCAAGAGGAGGCAAGGCCACATTGTCGCCATCAGCAGCATCCAGGGCAAG
ATGAGCATTCCTTTTCGATCAGCATATGCAGCCTCCAAGCACGCAACCAGGCTTTCTTTGA
CTGTCTGCGTGCCGAGATGGAACAGTATGAAATTGAGGTGACCGTCATCAGCCCCGGCTACA
TCCACACCAACCTCTCTGTAATGCCATCACCGCGGATGGATCTAGGTATGGAGTTATGGAC
ACCACCACAGCCAGGGCCGAAGCCCTGTGGAGGTGGCCAGGATGTTCTTGCTGCTGTGGG
GAAGAAGAAGAAAGATGTGATCCTGGCTGACTTACTGCCTTCCTTGGCTGTTTATCTTCGAA
CTCTGGCTCCTGGGCTCTTCTTCAGCCTCATGGCCTCCAGGGCCAGAAAAGACGGAAATCC
AAGAACTCCTAGTACTCTGACCAGCCAGGGCCAGGGCAGAGAAGCAGCACTCTTAGGCTTGC
TTACTCTACAAGGGACAGTTGCATTTGTTGAGACTTTAATGGAGATTTGTCTCACAAGTGGG
AAAGACTGAAGAAACACATCTCGTGAGATCTGCTGGCAGAGGACAATCAAAAACGACAACA
AGCTTCTTCCAGGGTGAGGGGAAACACTTAAGGAATAAATATGGAGCTGGGGTTTAACACT
AAAAACTAGAAATAAACATCTCAAACAGTAAAAAAAAAAAAAAAAAGGGCGGCCGCACTCTAG
AGTCGACCTGCAGAAGCTTGGCCGCCATGGCCCAACTTGTATTATGCAGCTTATAATGGTTAC

FIGURE 56

MDFITSTAILPLLFGCLGVFGLFRLLQWVRGKAYLRNAVVVITGATSGLGKECAKVFYAAGA
KLVLCGRNGGALEELIRELTASHATKVQTHKPYLVTFDLTDSGAIVAAAAEILQCFGYVDIL
VNNAGISYRGTIMDTTVDVDKRVMETNYFGPVALTKALLPSMIKRRQGHIVAIISSIQGKMSI
PFRSAYAASKHATQAFFDCLRAEMEQYEIEVTVISPGYIHTNLSVNAITADGSRYGVMDDTTT
AQGRSPVEVAQDVLAAVGGKKKDVILADLLPSLAVYLRLTAPGLFFSLMASRARKERKSKNS

Signal sequence:

amino acids 1-21

Transmembrane domain:

amino acids 104-120, 278-292

N-glycosylation site.

amino acids 228-232

Glycosaminoglycan attachment site.

amino acids 47-51

Casein kinase II phosphorylation site.

amino acids 135-139, 139-143, 253-257

Tyrosine kinase phosphorylation site.

amino acids 145-153, 146-153

N-myristoylation site.

amino acids 44-50, 105-111, 238-244, 242-248, 291-297

Amidation site.

amino acids 265-269

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 6-17

FIGURE 57

CCCACGCGTCCGCTGGTGTAGATCGAGCAACCCCTCTAAAAGCAGTTTAGAGTGGTAAAAAA
AAAAAAAACACACCAAACGCTCGCAGCCACAAAAGGGATGAAATTTCTTCTGGACATCCTC
CTGCTTCTCCCGTTACTGATCGTCTGCTCCCTAGAGTCCCTCGTGAAGCTTTTATTCTCTAA
GAGGAGAAAATCAGTACCGGCGAAATCGTGCTGATTACAGGAGCTGGGCATGGAATGGGA
GACTGACTGCCTATGAATTTGCTAAACTTAAAAGCAAGCTGGTTCTCTGGGATATAAATAAG
CATGGACTGGAGGAAACAGCTGCCAAATGCAAGGGACTGGGTGCCAAGGTTCCATACCTTTGT
GGTAGACTGCAGCAACCGAGAAGATATTACAGCTCTGCAAAGAAGGTGAAGGCAGAAATTG
GAGATGTTAGTATTTTAGTAAATAATGCTGGTGTAGTCTATACATCAGATTTGTTTTGCTACA
CAAGATCCTCAGATTTGAAAAGACTTTTGAAGTTAATGTACTTGCACATTTCTGGACTACAAA
GGCATTCTCTCCTGCAATGACGAAGAATAACCATGGCCATATTGTCACTGTGGCTTCGGCAG
CTGGACATGTCTCGGTCCCTCTTACTGGCTTACTGTTCAAGCAAGTTTGTCTGTGTTGGA
TTTCATAAAACTTTGACAGATGAACTGGCTGCCTTACAAATAACTGGAGTCAAAACAACATG
TCTGTGTCCTAATTTCTGTAACACTGGCTTCATCAAAAATCCAAGTACAAGTTTGGGACCCA
CTCTGGAACCTGAGGAAGTGGTAAACAGGCTGATGCATGGGATTCTGACTGAGCAGAAGATG
ATTTTTATTCCATCTTCTATAGCTTTTTTAAACAACATTGGAAGGATCCTTCTGAGCGTTT
CCTGGCAGTTTTAAAACGAAAAATCAGTGTTAAGTTTGATGCAGTTATTGGATATAAAATGA
AAGCGCAATTAAGCACCTAGTTTTCTGAAAACAGATTACCAGGTTTAGGTTGATGTCATCTA
ATAGTGCAGAAATTTAATGTTTGAACCTCTGTTTTTTCTAATTATCCCCATTTCTTCAATA
TCATTTTGTAGGCTTTGGCAGTCTTCATTTACTACCAGTGTCTTTAGCCAAAAGCTGATT
ACATATGATATAAACAGAGAAATACCTTTAGAGGTGACTTTAAGGAAAATGAAGAAAAGAA
CCAAAATGACTTTATTAAATAATTTCCAAGATTATTTGTGGCTCACCTGAAGGCTTTGCAA
AATTTGTACCATAACCGTTTATTAAACATATATTTTATTTTGTGATGCACTTAAATTTGT
ATAATTTGTGTTTCTTTTCTGTCTACATAAAATCAGAAACTTCAAGCTCTCTAAATAAAA
TGAAGGACTATATCTAGTGGTATTTACAATGAATATCATGAACTCTCAATGGGTAGGTTTC
ATCCTACCCATTGCCACTCTGTTTCCCTGAGAGATACCTCACATTCCAATGCCAAACATTTCT
GCACAGGGAAGCTAGAGGTGGATACCGTGTGCAAGTATAAAAGCATCACTGGGATTTAAG
GAGAATTGAGAGAATGTACCCACAAATGGCAGCAATAATAAATGGATCACACTTAAAAAAA
AA
AA

FIGURE 58

MKFLLDILLLLPLLVCSLESFVKLFIPKRRKSVTGEIVLITGAGHGIGRLTAYEFAKLKSK
LVLWDINKHGLEETAACKCKGLGAKVHTFVVDCSNREDIYSSAKVKAEIGDVSILVNNAGVV
YTSDLFATQDPQIEKTFEVNVLAHFWTTKAFLPAMTKNNHGHIVTVASAAGHVSVPFLLAYC
SSKFAAVGFHKTLTDELAALQITGVKTTCLCPNFVNTGFIKNPSTSLGPTLEPEEVNRLMH
GILTEQKMIFIPSSIAFLTTLERILPERFLAVLKRKISVKFDAVIGYKMQAQ

Signal sequence:

amino acids 1-19

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 30-34, 283-287

Casein kinase II phosphorylation site.

amino acids 52-56, 95-99, 198-202, 267-271

N-myristoylation site.

amino acids 43-49, 72-78, 122-128, 210-216

FIGURE 59

CCCACGCGTCCGCGGACGCGTGGGTCGACTAGTTCTAGATCGCGAGCGGCCGCCCGCGGCTC
AGGGAGGAGCACCAGCTGCGCCGCAACCTTGAGAGATGGGTTGGTGCCATGTGGAAGGTGATTG
TTTCGCTGGTCTGTGATGCTGGCCCCGTGTGATGGGCTGTTTCGCTCCCTATACAGAAGT
GTTTCCATGCCACCTAAGGGAGACTCAGGACAGCCATTATTTCTCACCCCTTACATTGAAGC
TGGGAAGATCCAAAAGGAAGAGAATTGAGTTTGGTCGGCCCTTTCCAGGACTGAACATGA
AGAGTTATGCCGGCTTCTCACCGTGAATAAGACTTACAACAGCAACCTCTTCTCTGGTTT
TTCCAGCTCAGATACAGCCAGAAGATGCCCCAGTAGTTCTCTGGCTACAGGTTGGGCCGGG
AGGTTTCATCCATTGTTGGACTCTTTGTGGAACATGGGCCTTATGTTGTACAAAGTAACATGA
CCTTGGCGTACAGAGACTTCCCCCTGGACCACAACGCTCTCCATGCTTTACATTGACAATCCA
GTGGGCACAGGCTTCAGTTTTACTGATGATACCCACGGATATGCAGTCAATGAGGACGATGT
AGCACGGGATTTATACAGTGCACTAATTTCAGTTTTTCAGATATTTCTGAAATATAAAAAATA
ATGACTTTTATGTCACTGGGGAGTCTTATGACAGGAAAATATGTGCCAGCCATTGACACCTC
ATCCATTCCCTCAACCTGTGAGAGAGGTGAAGATCAACCTGAACGGAATTGCTATTGGAGA
TGGATATTCTGATCCGGAATCAATTATAGGGGGCTATGCAGAAATCCTGTACCAAATGGCT
TGTTGGATGAGAAGCAAAAAAGTACTTCCAGAAGCAGTGCCATGAATGCATAGAACACATC
AGGAAGCAGAAGTGGTTTGAGGCTTTGAAATACTGGATAAACTACTAGATGGCGACTTAAC
AAGTGATCCTTCTTACTTCCAGAATGTTACAGGATGTAGTAATTACTATAACTTTTTGCGGT
GCACGGAACCTGAGGATCAGCTTTACTATGTGAAATTTTGTCACTCCAGAGGTTGAGACAA
GCCATCCACGTTGGGAATCAGACTTTAATGATGGAACATAGTTGAAAAGTACTTGGCAGA
AGATACAGTACAGTCACTTAAGCCATGGTTAACTGAAATCATGAATAATTATAAGGTTCTGA
TCTACAATGGCCAACTGGACATCATCGTGGCAGCTGCCCTGACAGAGCGCTCCTTGATGGGC
ATGGACTGGAAAGGATCCAGGAATACAGAAGGCAGAAAAAAAGTTTGGAAAGATCTTTAA
ATCTGACAGTGAAGTGGCTGGTTACATCCGGCAAGCGGGTGACTTCCATCAGGTAATTATTCT
GAGGTGGAGGACATATTTTACCCTATGACCAGCCTCTGAGAGCTTTTGACATGATTAATCGA
TTCATTTATGGAAGGATGGGATCCTTATGTTGGATAACTACTCCTCCAAAAGAGAACAT
CAGAGGTTTTATTGCTGAAAAGAAAATCGTAAAAACAGAAAATGTCTAGGAATAAAAAAA
TTATCTTTTATATCTGCAAGATTTTTTTCATCAATAAAAAATTATCCTTGAAACAACTGAGC
TTTTGTTTTTGGGGGAGATGTTTACTACAAAATTAACATGAGTACATGAGTAAGAATTACA
TTATTTAACTTAAAGGATGAAAGGTATGGATGATGTGACACTGAGACAAGATGTATAAAATGA
AATTTTAGGGTCTTGAATAGGAAGTTTTAATTCTTCTAAGAGTAAGTGAAAAGTGCAGTTG
TAACAAACAAAGCTGTAACATCTTTTCTGCCAATAACAGAAGTTTGGCATGCCGTGAAGGT
GTTTGGAAATATTATTGGATAAGAATAGCTCAATTATCCAAATAAATGGATGAAGCTATAA
TAGTTTTTGGGAAAAGATTCTCAAATGTATAAAGTCTTAGAACAAAAGAATTCTTTGAAATA
AAAATATTATATATAAAGTAAAAA

FIGURE 60

MVGAMWKVIVSVLVLMPGCDGLFRSLYRSVSMPPKGDGQPLFLTPYIEAGKIQKGRELSL
VGPPFGLNMKSYAGFLT VNKTYNSNLFFWFFPAQIQPEDAPVVLWLQGGPGGSSMFGLFVEH
GPVYVTSNMTLRDRDFPWTTLTSLMLYIDNPVGTGFSFTDDTHGYAVNEDDVARDLYSALIQF
FQIFPEYKNNDFYVTGESYAGKYVPAIAHLIHS LNPVREV KINLNGIAIGDGYSDPESIIGG
YAEFLYQIGLLDEKQKKYFQKQCHECIEHIRKQNWFEAFEILDKLLDGLTSDPSYFQNVGT
CSNYYNFLRCTEPEDQLYVVKFLSLPEVRQAIHVGNQTFNDGTIVEKYLREDTVQSVKPWLT
EIMNNYKVLIIYNGQLDIIVAAALTERS LMGMDWKGSGQEYKKAEEKVWKIFKSDSEVAGYIRQ
AGDFHQVIIRGGGHILPYDQPLRAFDMINRFIYGKGWDPPYVG

Signal sequence:

amino acids 1-22

N-glycosylation site.

amino acids 81-85, 132-136, 307-311, 346-350

Casein kinase II phosphorylation site.

amino acids 134-138, 160-164, 240-244, 321-325, 334-338, 348-352,
353-357, 424-428

Tyrosine kinase phosphorylation site.

amino acids 423-432

N-myristoylation site.

amino acids 22-28, 110-116, 156-162, 232-238

Serine carboxypeptidases, serine active site.

amino acids 200-208

Crystallins beta and gamma 'Greek key' motif signature.

amino acids 375-391

[illegible]

CGAGGGCTTTTCCGCGCCGGAATGGCACATGTGGGAATCCAGTCTTGTGGCTACAACAT
TTTTCCCTTCTCTAACAGTTTCTAACAGTCTTCTAACAGTCACTGAGTCAGGGGTTCTTCTT
CTGGGAGAAGAAAGGCTGAGGCGAGAGCAGGGCAGCTCTCACTAGGTGAGCAGGCTCTTGT
CCTCTCTGTGGATAACACAGACGATGAGAAAGTGAAGAGATGCAGCGGAGTGAGGTGATGGAAG
TCTAAATAGGAGAAGAAATTTTGTGTCAATATCAGACTCTGGGAGCAGTGTACCTGGAGAGC
CTGGGGGAGGGCTTGCCTTAACAGCTTTTAAAAAACAGGAGCGACTTCCATCTGGGCTGGAT
AAGACGTGCGCGGTAGATAGGGAAGTCTGGTTTAGTCTTAATATCAAAATGACTGGCTGG
TGAACTTCAACAGCCTTTTAACTCTCTGGAGATGAAACAGTGGCTTAAAGGGCCAGAA
TAGAGATGCTTTGTAAATAAAATTTTAAAAAAAGCAATGTTTATAGCTAAAGGCTAGA
GACCAAAATAGATAACAGGATTTGCTGAACATTTCTAAGAGGGGAGAAGATGTTTAAAAATA
GAAAAACCAAAATGCGAGAAGGAGGAGACTCACAGAGCTAAACAGGATGGGCACTTGGGTC
AGGCCAGCCTCTTGTGCTCTCTCCCGGAAATTTTGTGTGACCACTCTGCCTTGTGTTTT
CGAAGATCATGTGAGGGCCACCGGGGAGGTGGAGCAGATGAGCAACACAGGAGCCGCTCT
CCTCACCGCGCGCTCTCAGCATGGAAAGAGGAGCCCTGGCCCGGGCCCTGGAGGTGG
ACAGCGCCTCTGTGGCTCTGCTCTCAGTGGTCTGGGTGCTGCTGGTCCCCCAGCAGCGGC
ATGCTCTCAGTTTGCACACCTTCCACTCTAGAATGCTGACTGTGACCTTCAACCACTTGACCGT
CCACCAGGAGGACGGGGCCGTCTATGTGGGGGCCATCAACCGGGTCTAAAGCTGACAGGCA
ACCTGACCATCCAGGTGGCTCTAATAGACAGGGCCAGAGAAGGACCAACAGTCTCGTTAACCCG
CCCTCATCTGTCGACCTCTGACGGCAAGTGCTCACCTTCAACCAATGTCAACAGACTGCT
CATCATTTGACTACTCTGAGAAGCCGCTGCTGGCTGTGGGAGCTCTACCAAGGGGTCTGCA
AGCTGCTGGCGGTGGATGACCTTCTTCACTCTGGTGGAGCCATCCCAAGAAGGAGCATAC
CTGTCCAGTGTCAACAAGACGGGCACCATGTACGGGGTGATTGTGCGCTCTGAGGGTGAGGA
TGGCAAGCTTCTCATCGGCACGGCTGTGGATGGGAAGCAGGATTACTTCCCGAGTGTCTCA
CGCGAAGTGTCCCGGAGACCTTGAAGTCTCAGGAGTGTGCAATGAGCTACACAGGAT
TTTGTCTCTCTCTCATCAAGATCCCTTCAGACACCCCTGGCCCTGGTCTCCCACCTTGACAT
CTTCTACATCTACGCTTTTGCTAGTGGGGCTTTGTCTACTTTCTCACTGTCTCAGCCCGAGA
CCCCTGAGGGTGTGGCCATCAACTCCGTGGAGACCTTCTACACCTACGCTATCTGTCGG
CTTGTCAAGGATAGCCCAAGTCTTCACTCATAGCTGTCCCTGCTCCGTCTCGGCTGCAACCGGG
CGGGGTGGAATACCGCTCTGTCGAGCTGTACTCTGCGCAAGCTGGGAGCTCACTGGCCC
AGGCCTTCAATATCACAGGACGAGCGATGTACTCTTTGGCCATCTTCTCCAAAGGCGAGAAG
CAGTATCACCAACCCCGGAGTACTTGCCCTGTGTGCTCTCCCTATCGGCGCATCAACTT
CGAGATCAAGGAGCGCTCGACTCTGTCTACAGGGCGAGGGCAACCTGGAAGCTCAACTGGC
TGCTGGGGAAGGACGTCCAGTGCAGCAAGGCGCTGTCCCATGCGATGATTAATCTCTGTGGA
CTGGACATCAACAGCCCTGGGAGCTCAACTCAGTGTGAGGGCCTGACCTGTACACCAC
CAGCAGGAGCCGATGACCTCTGTGGCCCTCTACGTTTACAACGGGTACAGCGTGGTTTTTG
TGGGAGCTAAGAGTGGCAAGTGTAAAAAGGTAAAGTCTATGAGTTGAGATGCTCCCAATGCC
ATTCACTCTCTGAGCAAGAGTCCCTCTTGAAGGTAGCTATTGGTGGAGATTAACTATATAG
GCAACTTTATTTCTTGGGGAACAAGGCTGAAGTGGGAGGTGAAGAGGGGTTAAATTTTGTG
AATTAGCTTCTAGCTACTCTCCCTCAGGCATCAGTCACTTGGGTATGTAAGAAAGTCAAGCGTA
TTTCAATATTTCCAAACTTTAAGAAAACCTTTAAGAAAGTACATCTGCAAGGACAA

FIGURE 62

MGTLGQASLFAPPNGYFWSHSAFCFAESCEGQPGKVEQMSTHRSRLTTAAPLSMEQRQPWP
RALEVDSSRSVLLSVVWVLLAPPAAGMPQFSTFHSENRDWTFNHLTVHQGTGAVYVGAINRV
YKLTGNLTIQVAHKTGPEEDNKSRYPLIVQPCSEVLTLTNVVKLLIIDYSENRLACGSL
YQGVCKLLRLDDLFI LVEPSHKKEHYLSSVNKTGTMYGVIVRSEGEDGKLFIGTAVDGGKQDY
FPTLSSRKLPDPRESSAMLDYELHSDFVSSLIKIPSDTLALVSHFDIFYIYGFASSGGFVYFL
TVQPETPEGVAINSAAGDLFYTSRIVRLCKDDPKFHSYVSLPFGCTRAGVEYRLLQAAYLAKP
GDSLAQAFNITSQDDVLFALFISKGQKQYHHPPDDSAALCAFPPIRAINLQIKERLQSCYQGEGN
LELNWLLGKDVQCTKAPVPIDNFCGLDINQPLGGSTPVEGLTLYTTSRDRMTSVASYVYNG
YSVVVFGTKSGKLLKVRVYEFRCNSNAIHLSSKESLLEGSYWWRFNYRQLYFLGEQR

Signal sequence:

amino acids 1-32

Transmembrane domain:

amino acids 71-87

N-glycosylation site.

amino acids 130-134, 145-149, 217-221, 381-385

Casein kinase II phosphorylation site.

amino acids 139-143, 229-233, 240-244, 291-295, 324-328, 383-387,
384-388, 471-475, 481-485, 530-534

N-myristoylation site.

amino acids 220-226, 319-325, 353-359, 460-466, 503-509

FIGURE 63

AGGCTCCCGCGCGCGCTGAGTSCGGACTGGAGTGGGAACCCGGGTCCCCGCGCTTAGAGAACACGCGCATGACCA
CGTGGAGCCTCCGCGGAGGCGCGGCCCGCAGCTGGGACTCCTGTGCTGTGTCGCTTTGGGCTTCCTGGTGTCTCC
GCAGSCTGGACTGGAGCACCCTGGTCCCTCTGCGGCTCCGCCATCGACAGCTGGGGCTCGAGGTCACAGGCGTGGGA
ACTTCATGCTCGAGGAGTCCACCTTCTGGGATCTTCGGGGGCTCCATCCACTATTTCGCTGTGTCGAGGAGTACT
GGAGGGACCGCTGCTGAAGATGAAGGCTGTGGGCTTGAAACCCCTCACCACTATGTTTCCGTGGAACTTGCATG
AGCCAGAAAGAGGCAAAATTGACTTCTCTGGGAACCTGGACCTGGAGGCTTCTGTCCTGATGGCGCCAGAGATCG
GGCTGTGGGTGATTCTGCGCTCCAGGCCCTCATCTGCAGTGAGATGGACCTCGGGGGCTTCGCCAGCTGGGTAC
TCCAAGACCTTGGCATGAGGCTGAGGCAACTTACAAGGGCTTACCCGAAGCAGTGGACCTTTATTTTGAACACC
TGATGTCCAGGCTGGTGCCTCCAGTACAAGCCTGGGGGACCTATCATTTGCCGTGAGTGGAGATGAATATG
GTTCCTATAAATAAGACCCCGCATACATGCCCTACGTCAAGAAGGCATGGAGGACCTGGGCACTTTGGAACTGC
TCTGACTTCAGACAACAGGATGGGCTGAGCAAGGGGATTGTCCAGGAGTCTTGGCCCACTCAACTTCAGT
CAACACACAGCTGCAGCTACTGACCACCTTTCTCTTCAACGTCCAGGGGACTCAGCCCAAGATGGTGTGAGT
ACTGGACGGGTGGTTTGTACTCTGCGGGAGGCCCTCACAAATATCTTGGATTCTTCTGAGGTTTTGAAAACCGTGT
CTGCCATTGTGGACCGCGCTCCTCCATCAACCTCTACATGTTCCACGGAGGCACCACTTTGGCTTCATGAATG
GAGCCATGCACCTTCCATGACTACAAGTCAGATGTCAACAGCTATGACTATGATGCTGTGCTGACAGAAAGCCGCG
ATTACAGGCCAAGTACATGAAGCTTCGAGACTTCTCGGCTCCATCTCAGGCACTCCTCTCCCTCCCCACCTG
ACCTTCTTCCCAAGATGCGTATGAGCCCTTAAACCGCAGTCTTGTAACCTGTCTCTGTGGGACGCCCCCAAGTACC
TGGGGAGGCAATCAAGTCTGAAGGCCCATCAACATGGAGAACCTGCCAGTCAATGGGGGAAATGGACAGTCTCT
TCGGGTACATTCTCTATGAGACCAGCATCACTCGTCTGGCATCCTCAGTGGCCAGTGCATGATCGGGGGCAGG
TGTTTGTGAACACAGATATCCATAGGATCTTGGACTACAAGCAACAGAGATTGCTGTCCCCCTGATCCAGGGT
ACACCGTGTGAGGATCTTGTGGAGAACTCGTGGCGGAGTCAACTGTGGGGGAGAAATATTGATGACCCAGCGAAAG
GCTTAATTGAGAAATCTCTATCTGAATGATTCAACCCCTGAAAACCTCTCAGAACTCTATAGCTGGATTAAGAAAG
GCTTTCTTTCAGAGGTTTCGCGCTGAGCAAAATGNGTTCCTCCCGAGAAACCCACATTACCTGCTTCTTCTTGG
GTAGCTTGTCCATCAGCTCCACGCTTGTGACACCTTTCTGAAGCTGGAGGGCTGGGAGAAAGGGGTTGATATCA
TCAATGGCCAGAACTTCAGCGTTACTTGAAACATTTGGACCCCAAGAAAGCGTTTACCTCCAGGTCCTGTGTGA
GCAGGGAATCAACAGGTCATCGTTTTGAGGAGACAGTGGCGGCCCTCAGTTACAGTTTACGGAAACCCCC
ACCTGGGCAAGAACAGTACATTAGTGGCGGTGGCACCCCTCCTGCTGTGTGCCAGTGGGAGACTGCGCGCTC
CTCTTGA CTTGAAGCTGTGGGCTGCTGCCCCACCCCTCACTGCAAAAGCATCTCCTTAAGTAGCAACCTCAGG
ACTGGGGCTACAGTCTGCCCTGTCTCAGCTCAAAACCTTAAGCCTGCAGGGAAGGTGGGATGCTCTGGGCC
TGGCTTTGTGTATGATGGCTTCTACAGCCCTGCTCTTGTGCCAGGCTGTGCGGCTGTCTCTAGGGTGGGAGC
AGCTAATCAGATCGCCAGCCTTGGGCCCTCAGAAAAAGTGTGAAACGTGCCCTTGCACGGACGTCAAGCCC
TGCAGCATCTGTGGACTCAGGCGTGTCTTTGCTGGTTCTGGGAGGCTTGGCCACATCCCTCATGGCCCAT
TTTATCCCCGAAATCTCGGTGTGTCAACAGTGTAGAGGCTGGGGAAGGGGTGTCTCACCTGAGCTGACTTTGTT
CTTCTTCAACACCTCTGAGCCTTCTTTGGGATCTGGAAGGAACCTCGCGTGGAGAACATGTGCTTCCCCCT
TCCCTTCCACTCGTGTCTTCCACAGGGTGA CAGGCTGGGCTGGGAGAACAGAAATCTCACCTGCGCTTCC
CAAGTTAGCAGGTGCTCTGTGTCTCAGTGAGGAGGACATGTGACTCTGCGCAGAAAGCCATGGCCATGTGCA
CATCCAGGGAGGAGGACAGAAAGCCAGCTCACATGTGAGTCTTGGCAGAAAGCATGGCCCATGTCTGCACATCC
AGGAGGAGGAGCAGAAAGCCAGCTCACATGTGAGTCTTGGCAGAAAGCCATGGCCCATGTCTGCACATCCAGGAGG
ACAGAAAGGCCCTCAGTGGCCCCGCTCCCCACCCCCACGCGCGAAGCAGGGGGCAGAGCAGCTCTTCTG
GAAGTGTGTCCAAGTCGCAATTTGAGCCTTGTCTGGGGCCAGCCCAACACCTGGCTTGGGCTCAGTCTCTGA
GTTGCAGTAAAGCTATAACCTTGAATCAAA

FIGURE 64

MTTWSLRRRPARTLGLLLLVLGFLVLRRLDWSTLVPLRLRHRQLGLQAKGWNFMLEDSTFW
IFGGSIHYPFRVPREYWRDRLLKMKACGLNTLTITYVPWNLHEPERGKFDFSGNLDLEAFVLMA
AEIGLWVILRPGPYICSEMDLGGLP SWLLQDPGMRLRTTYKGFTAVDLYFDHLMSRVVPLQ
YKRGFP IIAVQVENEYGSYNKDPAYMPYVKKALEDRGIVELLLTSDNKDGLSKGIVQGVLAT
INLQSTHELQLLTTFLENVQGTQPKMVM EYWTGWFD SWGGPHNILD SSEVLKTVSAIVDAGS
SINLYMFHGGTNFGFMNGAMHFHDYKSDVTSYDYDAVLTEAGDY TAKYMKLRDFFGSISGIP
LPPPPDLLPKMPYEPLTPVLYLSLWDALKYLGEPIKSEKPINMENLPVNGGNGQSFGYILYE
TSITSSGILSGHVHDRGQVFVNTV SIGFLDYKTTKIAVPLIQGYTVLRI LVENRGRVNYGEN
IDDQRKGLIGNLYLNDSP LKNFRIYS LDMKKSFFQRFGLDKWXS LPEPTLPAPFFLGSL SIS
STPCDTFLKLEGWEKG VVFINGQNLGRYWNIGPQKTL YLPGPWLSSGINQVIVFEETMAGPA
LQFTETPHLGRNQYIK

Signal sequence:

amino acids 1-27

Casein kinase II phosphorylation site.

amino acids 141-118, 253-257, 340-344, 395-399, 540-544, 560-564

N-myristoylation site.

amino acids 146-152, 236-242, 240-246, 244-250, 287-293, 309-315,
320-326, 366-372, 423-429, 425-431, 441-447, 503-509, 580-586

FIGURE 65

GGGGACGCGGAGCTGAGAGGCTCCGGGCTAGCTAGGTGTAGGGGTGGACGGGTCCAGGACC
 CTGGTGAGGGTTCTCTACTTTGGCCCTTCGGTGGGGGTCAAGACGCGAGGCACCTACGCCAAAGG
 GGAGCAAAGCCGGGCTCGGCCCGAGGCCCCAGGACCTCCATCTCCCAATGTTGGAGGAATC
 CGACACGTGACCGTCTGTCCGCCGTCTCAGACTAGAGGAGCGCTGTAAACGCCATGGCTCCC
 AAGAAGCTGTCTGCGCTTCGTTCCCTGCTGCTGCCGCTCAGCCTGACGCTACTGCTGCCCA
 GGCAGACACTCGGTGCTTCGTAGTGGATAGGGGTCTGACCGGTTCTCTAGACGGGGCCC
 CGTTCCCGCTATGTGTCTGGCAGCCTGCACCTACTTTCCGGTACC CGGGGTGCTTTGGGCCGAC
 CGGCTTTTGAAGATGCGATGGAGCGGCCCTCAACGCCATACAGTTTATGTGCCCTGGAACCTA
 CCACGAGCCACAGCCTGGGGTCTATAACTTTAATGGCAGCCGGACCTATTGCCCTTCTGA
 ATGAGGCGAGCTCTAGCGAACCTGTGGTCATACTGAGACCGAGGACCTTACATCTGTGCAGAG
 TGGGAGATGGGGGCTCTCCCATCTGGTTGCTTCGAAAACCTGAAATTCATCTAAGAACCTC
 AGATCCAGACTTCCTTGCCGCGAGTGGACTCTGGTTCAAGGTCTTGTGCCCCAAGATATATC
 CATGGCTTTATCACAATGGGGGCAACATCATTAGCATTACGGTGGAGAAATGAATATGGTAGC
 TACAGAGCCTGTGACTTCAGCTACATGAGGCACCTGGCTGGGCTCTCCGTCGACTGCTAGG
 AGAAAAGATCTTGCTCTTACCACAGATGGGCCCTGAAGGACTCAAGTGTGGCTCCCTCCGGG
 GACTCTATACCACTGTAGATTTTGGGCCAGCTGACACATGACCAAAATCTTACCTGCTT
 CGGAAGTATGAACCCCATGGGCCATTGGTAAACTCTGAGTACTACACGGCTGGCTGGATT
 CTGGGGCCAGAACTACTCCACACGGTCTGTGTGCTGAGCTGTAAACCAAGGACTAGAGAACATGC
 TCAAGTTGGGAGCCAGTGTGAACATGTACATGTTCCATGGAGGTACCAACTTGGATATTGG
 AATGGTGGCGATAAGAAGGGACGCTTCCTCCGATTACTACCAGCTATGACTATGATGCACC
 TATATCTGAAGCAGGGGACCCACACCTAAGCTTTTGTGCTTCGAGATGTATCAGCAAGT
 TCCAGGAAGTTCTTTGGGACCTTACCTCCCCGAGCCCCAAGATGATGCTTGGACCTGTG
 ACTCTGCACCTGGTTGGGCATTTACTGGCTTCTAGACTTGTCTTGCCCCGTGGGCCCAT
 TCAATCAATCTTGCCAATGACCTTTGAGGCTGTCAAGCAGGACCATGGCTCATGTTGTACC
 GAACCTATATGACCCATACCATTTTGTAGCCAAACACCTATTCTGGGTGCCAAATATGGAGTC
 CATGACCGTGCCATGTGATGGTGGATGGGGTGTTCAGGGGTGTGTGGAGCGAAATATGAG
 AGACAAACTATTTTTCAGCGGGGAACTGGGGTCCAACTGGATATCTTGGTGGAGAACATGG
 GGAGGCTCAGCTTTGGGTCTAACAGCAGTGACTTCAAGGGCCTGTTGAAGCCACCAATTCTG
 GGGCAACCAATCTCTACCAATGGATGATGTTCCCTCTGAAAATTGATAACCTTGTGAAGTG
 GTGGTTTCCCTCCAGTTGCCAAAATGGCCATATCTCAAGTCCTTCTGGCCCCACATTCT
 ACTCCAAACATTTTCCAATTTTGGCTCAGTTGGGGACACATTTCTATATCTACCTGGATGG
 ACCAAGGGCCAAGTCTGGATCAATGGGTTTAACTTGGGCGGTACTGGACAAAGCAGGGGCC
 ACAACAGACCCCTCTACGTGCCAAGATTCTGCTGTTTCTAGGGGAGCCCTCAACAAAATTA
 CATTGCTGGAAGTGAAGATGTACCTCTCAGCCCCAAGTCCAATTTTGGATAAGCCTATC
 CTCAAATAGCACTAGTACTTTTGCACAGGACACATATCAATTCCCTTTCAGCTGATACACTGAG
 TGCTCTGAACCAATGGAGTTAAGTGGGCACCTGAAGGTAGGCGGGGATGTTGGCTCATGC
 CTGTAATCCCCAGCACTTTGGGAGGCTGAGACGGGTGGATTACCTGAGGTGAGGACTTCAAGA
 CCAGCCTGGCCCAACATGGTGAACCCCGTCTCCACTAAAAATACAAAATTAGCCGGCGGTG
 ATGGTGGGCACCTCTAATCCAGCTACTTGGGAGGCTGAGGGCAGGAGAATTGCTTGAATCC
 AGGAGGCAGAGGTTGCAGTGAGTGGAGGTTTACCACCTGCACTCCAGCCTGGCTGACAGTGA
 GACACTCCATCTCAAAAAAAAAA

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FIGURE 66

MAPKKLSCLRSLLLPLSLTLLLPQADTRSFVVDRGHDRFLLDGAPFRYVSGSLHYFRVPRVL
WADRLLKMRWSGLNAIQFYVPWNYHEPQPGVYNFNGSRDLIAFLNEAALANLLVILRPGPYI
CAEWEMGGPLPSWLLRKPEIHLRTSDPDFLAAVDSWFKVLLPKIYPWLYHNGGNIISIQVENE
YGSYRACDFS YMRHLAGLFRALLGEKILLFTTDGPEGLKCGSLRGLYTTVD FGPADNMTKIF
TLLRKYEPHGPLVNSEYYTGWLDYWGQNHSTRSVSAVTKGLNMLKLGASVNMYPFHGGTNF
GYWNGADKKG RFLPITTSYDYDAPISEAGDPTPKLFALRDVISKFQEVPLGPLPPSPKMMML
GPVTLHLVGHLLAFLDLLCPRGPIHSILEPMTFEAVKQDHGFMLYRTYMTHTIFEPTFFWVFN
NGVHDRAYVMVDGVFQGVVERNMRDKLFLTGKLGSKLDILVENMGRLSFGSNS SDFKGLLKP
PILGQTILTQWMMFPLKIDNLVKWWFPLQLPKWPYPQAPSGPTFYSKTFPILGSVGD TFLYL
PGWTKGQVWINGFNLGRYWTKQGPQOTLVVPRLLFPRGALNKITLLEEDVPLQPQVQFLD
KPILNSTSTLHRTHINSL SADTLSASEPMELSGH

Signal sequence:

amino acids 1-27

N-glycosylation site.

amino acids 97-101, 243-247, 276-280, 486-490, 625-629

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 4-8

Casein kinase II phosphorylation site.

amino acids 148-152, 234-238, 327-331, 423-427, 469-473, 550-554,
603-607, 644-648

Tyrosine kinase phosphorylation site.

amino acids 191-198

N-myristoylation site.

amino acids 131-137, 176-182, 188-194, 203-209, 223-229, 227-233,
231-237, 274-280, 296-300, 307-313, 447-453, 484-490

FIGURE 67

GCTTTGAACACGCTCTGCAAGCCCAAGTTGAGCATCTGATTGGTTATGAGGTATTGAGTGC
ACCCACAATATGGCTTACATGTTGAAAAAGCTTCTCATCAGTTACATATCCATTATTGTGT
TTATGGCTTTATCTGCCTCTACACTCTCTTCTGGTTATTTCAGGATACCTTTGAAGGAATATT
CTTTGAAAAAGTCAGAGAAGAGAGCAGTTTGTAGTACATTCCAGATGTCAAAAACGATTTT
GCGTTCCTTCTTACATGGTAGACCAGTATGACCAGCTATATTCCAAGCGTTTGGTGTGTT
CTTGTGAGAAGTTAGTGAAAATAAACTTAGGGAAATAGTTTGAACCATGAGTGGACATTTG
AAAACTCAGGCAGCACATTTACGCAACGCCAGGACAAGCAGGAGTTGCATCTGTTTCATG
CTGTGCGGGGTGCCCGATGCTGTCTTTGACCTCAGAGACCTGGATGTGCTAAAGCTTGAAC
AATTCAGAGAAGCTAAAAATCCTGCTAAGATTCTCAAATGACTAACCTCCAAGAGCTCCACC
TCTGCCACTGCCCTGCAAAAGTTGAACAGACTGCTTTTAGCTTCTCTCGCGATCACTTGAGA
TGCTTTCACGTGAAGTTCAGTGATGTGGCTGAAATTCCTGCCTGGGTGTATTGTCTAAAAA
CCTTCGAGAGTTGTACTTAATAGGCAATTTGAACTCTGAAAACAATAAGATGATAGGACTTG
AATCTCTCCGAGAGTTGCGGCACCTTAAGATTCTCCAGTGAAGAGCAATTTGACCAAAGTT
CCCTCCAACATTACAGATGTGGCTCCACATCTTACAAGTTAGTCATTCATAATGACGGCAC
TAAACTCTTGGTACTGAACAGCCTTAAGAAAATGATGAATGTGCTGAGCTGGAACCTCCAGA
ACTGTGAGCTAGAGAGAATCCACATGCTATTTTCAGCCTCTCTAATTTACAGGAACCTGGAT
TTAAAGTCCAATAACATTGCGACAATTGAGGAAATCATCAGTTTCCAGCATTTAAAAACGACT
GACTTGTTTAAAAATTATGGCATAACAAAATTGTTACTATTCTCCCTCTATTACCCATGTCA
AAAACCTGGAGTCACTTTATTCTCTAACAACAAGCTCGAATCCTTACCAGTGGCAGTATTT
AGTTTACAGAAACTCAGATGCTTAGATGTGAGCTACAACAACATTTCAATGATTTCCAATAGA
AATAGGATTGCTTTCAGAACCTGCAGCATTTGCATATCACTGGGAACAAAGTGGACATTCTGC
CAAAACAATTTGTTTAAATGCATAAAGTTGAGGACTTTGAATCTGGGACAGAACTGCATCACC
TCACTCCCAGAGAAAGTTGGTCAGCTCTCCAGCTCACTCAGCTGGAGCTGAAGGGGAAGT
CTTGACCGCTGCCAGCCAGCTGGGCCAGTGTGCGATGCTCAAGAAAAGCGGGCTTGTG
TGGAAGATCACCTTTTGTATACCCTGCCACTCGAAGTCAAAGAGGCATTGAATCAAGACATA
AATATTCCCTTTGCAAAATGGGATTAAACTAAGATAATATATGCACAGTGATGTGCAGGAAC
AACTTCCTAGATTGCAAGTGCTCAGGTACAAGTTATTACAAGATAATGCATTTTAGGAGTAG
ATACATCTTTTAAAAATAAAACAGAGAGGATGCATAGAAGGCTGATAGAAGACATAACTGAAT
GTTCAATGTTGTAGGGTTTTAAGTCATTCATTTCCAATCATTTTCTTTCTTTTGGG
AAAGGGAAGGAAAAATTATAACTACTAATCTTGGTCTCTTTTAAATTGTTTGTAACTTGGAT
GCTGCCGCTACTGAATGTTTACAAATTGCTTGCTGCTTAAAGTAATGATTAAATTGACATT
TCTTACTAAAAA

FIGURE 68

MAYMLKKLLISYISIIICVYGFI~~C~~LYTLFWLFRIP~~L~~KEYSFEK~~V~~REESSFS~~D~~IPDVKNDFAPL
LHMVDQYDQLYSKRFGVFLSEVSENK~~L~~REISLNHEWTFEKL~~R~~QHISR~~N~~AQDKQELHLF~~M~~LSG
VPDAVFDLTDDLVLKLELIPEAKIPAKISQMTNLQELHLCHCPAKVEQTAFSFLRDHLRCLH
VKFTDVAEIPAWVYLLKNLRELYLIGNLSEN~~N~~KMIGLES~~L~~RELRLHLKI~~L~~HVKS~~N~~LTKVPSN
ITDVAPHLTKLVIHNDG~~T~~KLLVLNSLKKMMNVAE~~L~~ELQNC~~E~~LERIPHAIFSLSNLQELDLKS
NNIRTIEEIIISFQHLKRLTCLKLWHNKIVTIPPSITHVKNLES~~Y~~FSNNKLES~~L~~PVAVFSLQ
KLRLCDVSYNNISIM~~I~~PIEIGLLQNLQHLHITGNKVDILPKQLFKCIKLRTLNLGQNCITSLP
EKVGQLSQLTQLELKGNC~~L~~DRLPAQLGQCRMLKKSGLVVEDHLFD~~T~~LPLEVKEALNQDINIP
FANGI

Signal sequence:

amino acids 1-20

N-glycosylation site.

amino acids 241-245, 248-252, 383-387

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 326-330

Casein kinase II phosphorylation site.

amino acids 48-52, 133-137, 226-230, 315-319, 432-436, 444-448

Tyrosine kinase phosphorylation site.

amino acids 349-355, 375-381

N-myristoylation site.

amino acids 78-84, 124-130, 212-218, 392-398

Journal of Interpersonal Violence 26(10) 1991-2004
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DOI: 10.1177/0886260511417111
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CCACGCGCTCGGGCTGCTCTCTGGACCTTGGCAATTTCTCTTCTTTTCATTGACAACAACTGATTTTTTAATTCTCT
TTTTCATCTCTGTGGCCAGCTTGGGATCTAGSCGCCCTGGGAAGCAATTTGTGTTTACACACAATGAAGT
CTGTGTTTGGGGTCTTCTCTCTCCCTCCGACATTCAGTTCGTTAGTGTTGTGTGGGAGGGAGACACAGCTGG
CGTCAGTCTGCTGCTGCACTTATCGCTCAGGTACATCAGAGTCTTTGACCTCATACAGTGAATATGCTGCTGT
ATGCTGTGTGTATCTCTGGCGGCGCTTGTCTCTGCTGATAGTTGTGCTGCTGTCTTTTCTTCAATTAACAAC
AGCTCAAAAGCTGTCAARGAACTCTGAAGCTGTGGCTGTAAAAAATCACAAACGAGACAAAGTGTGGTGGGCGAAG
AACASCCAGGGCCAAACCAATGTGCCAGGAGTCTTGTCTGCCCTCGAGTGTGTGAAGATATAGAAATGTGTGT
AGTTTGTGATCTGCTGCCAATCTGCTGTTCGCACTAATAATAGGGCCCTCTGAGTATAGGAAGAGCTCCCTCTTCAAG
GTAGAGCTCTGAAGACTTCAATGATGTCAATGAGGCCACTGTTTTGTGATGTGACGAGCAAGAAAGGACAGT
CTCCATCGAGTCTTTCATCGAAAAATGTCAGTGCCTGTCTGGAAACAGCTGTCTGAGAGTCCCTTACAGAGAGCTTC
CTACGCGGGCAACTCTTCAGGAAGAGTGTGGGAGAGAGACCTCATCTGGGGAATGCTGATAAAACAGTCA
CACAGCTGCTCTATTTCACACAAATCACCCCTTCGCTGTGGTGGAAATGAGCTTCTCCCTGGAGGTGTCCAGAAA
GCTGATGTAAACACAGGCTCTATAAAGCTGTGGTCTTTAGGCTGCCAGCGCTTCGCAAAATGGAGCTTGTGTA
AGAGAGTCTGATCCGCAATGACCTCTTAATTTCTCTCTGTTCGTGGCGAGTGTGCAATCGCGGAGGCTGAAAGCAAT
CGAAGCTGCACAGTCAGTCTAGGGGTGGCAATATGCGAGACAGCAAAAGCCATGATCTGCAACTCAATCCC
AGTGAAGACTCGCACTGGACATAGAAAGACCAAAAAACAAAGCAATCAGAATATTCTTTTCTCATGTCCAGTCT
GTACCAAGTGGAACTGTGAAAGTGAAGAACTAAAGACTTTTGAACGGAATCTCAGCAACTGGGCTCTGTGTAGG
CAAGTCTGCAGTAAAAACGACTATGTTCTGTATTGTGAATCAATCTCAGTATGATGAGTTCCTCAAAATGATTCT
GATCAGACAGAATTAACAAGACTGTCTTGTCTCTCACTACTCTCTCTCTCTAACTCTCTATTTCGAAAGTGT
GGCGTCTCTCTGGATACCTTGAAGAACTCTTCACACGCCCAATTAACCAAGCGCGCTCTGAGTGGCTGTCT
TGTGTGTGGCCACATCAAGTGGAGAAGATTAACAGATATAAACTAAATCTAAAGAGATTTTCTAGAAAATAGAC
AACACAGTGCAAATTTGATTTCTTGCACATATGATGCCCTCCACAACTGTGGCTGATTCGACAGAGTCTGT
GGCGCTGTGACTCCCACTTCGAATCGCTATCAAACTCTCTGACTGTGCTGTGTCTACAGATTTGCAACTTGT
TACCGGGATTTCTGCTCTCTCACTCAATTAATGAGTGGCAAAAACTCAACATCAATTTTAACTGTCTCTCT
GACAGTGTGAGATTTATAGAACAATCTACTTAGAGGCTTTTAACTCTAATGGGAATACTGTGCAACTAAAA
GACCCAACTGCGACACAAAATTTATCAAATGTGTGGAAATTTCTGTCCTCTTAATGGATGTGGTACATCAAG
AAGTGTAGAAGTCACTCAATTACTTACCAAAATTAATCACTTTTCTGCACTCAAACTCTGAAGTGTACCG
CTGTGAAATCAATCCAGATATTGTGAAGTGTGAAATGGGACATAATTTCTACAGTGGAGATAATATACATCAAC
GAGATGTGTGTAATACAGAGTCAAAATGCACTGGGCAATAACACAGCACTGGCTCTTTTGTGATCCAACTTCA
TTGAAAGACATATATCTGAATCACATATATATGTGATTTGAAACAAACTCTTTTGTTCAGTGTAGTCTGTGAC
ACTCCAGATCAAAATTTGTGTGTGTTTCTGATATCTAGAGCTCTGCCAATCTGACTTTGTGACTCTCAACAA
TAGCACTTAATCAAGAGTGGATGTAGTCGAGATGAACCTGTGAAGTGTATCCCTTATTGTGACACATATGGGAGA
TTCCAGTTTAATGCTTTAAATTTCTGAGAAGTATGAGCTGTGTATCTGAGTGTAAAGTTTGTATGTGTAT
AACAGTGAACACAGCTCTCGCTGCAATCAAGTGTGTGTCTCGAAGAGCAACGAGCAATTTCTCATATAAAAGG
AAAACTGACTTCATCATAGAGCCACTTCTGTGAAAAGGAGTAGAGTCAAGTGCAGTTCAGGATTTTCAGAT
GAAACCACTCGGGAAGAAATCCAAACGAGCTTTTCAACAGTGTGCATCTTGTTCCTCATGGTCTTAGCTCTG
AATGTGGTGACTGTAGCGCAACTCAGATGAGGCAATTTGTGAATCAAGCGGAGACATCAAAATCAGAGAGTCT
CGACATCATTAATCAAGCTCCAACTCTAAGTAGACATCTCTCTCAGAGTGCCTCAAGGAAATGCTACTCGT
GGACTACATATATGAATAAATGAGGAAGGGCTGAAAGTGATCACACAGGCTGTGTAAAAAA

FIGURE 70

MELVRRMLPLTLLILSCLAELTMAEAEGNASCTVSLGGANMAETHKAMILQLNPSENCTWTI
ERPENKSIRIIIFSYVQLDDPGSCSENIKVFDGTSSNGPLLGGVCSKNDYVPVFESSSSSTLT
FQIVTDSARIQRTVFVFYFFSPNISIPNCGGYLDTLEGSFTSPNYPKHPPELAYCVWHIQV
EKDYKIKLNFKEIFLEIDKQCKFDFLAIYDGPSTNSGLIGQVCGRVTPTFESSSNSLTVVLS
TDYANSYRGFSASYTSIYAENINTTSLTCSSDRMRVLIISKSYLEAFNSNGNNLQLKDPTCRP
KLSNVVEFSVPLNGCGTIRKVEDQSITYTNIITFSASSTSEVITRQKQLQIIVKCEMGHNST
VEIIYITEDDDVIQSQNALGKYNTSMALFESNSFEKTILESPIYYVDLNQTLFVQVSLHTSDPN
LVVFLDTCRASPTSDFASTPYDLIKSGCSRDETCKVYPLFGHYGRFQFNAPKFLRSMSSVYL
QCKVLI CDSSDHQSRCNQGCVSRSKRDISSYKWKTDSSIIGPIRLKRDRSASGNSGFGQHETHA
EETPNQPFNSVHLFSFMVLALNVVTVATITVRHFVNQRADYKYQKLQNY

Signal sequence:

amino acids 1-24

Transmembrane domain:

amino acids 571-586

N-glycosylation site.

amino acids 29-33, 57-61, 67-71, 148-152, 271-275, 370-374,
394-398, 419-423

Casein kinase II phosphorylation site.

amino acids 22-26, 108-112, 289-293, 348-352, 371-375, 379-383,
408-412, 463-467, 520-524, 556-560

Tyrosine kinase phosphorylation site.

amino acids 172-180, 407-415, 407-416, 519-528

N-myristoylation site.

amino acids 28-34, 38-44, 83-89, 95-101, 104-110, 226-232

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 7-18

FIGURE 71

GACGGAAGAACAGCGCTCCCGAGGCCGCGGGAGCCTGCAGAGAGGACAGCCGGCCTGCGCCG
GGACATGCGGCCCCAGGAGCTCCCCAGGCTCGCGTTCCCGTGTGCTGTTGCTGTTGCTGC
TGCTGCCGCCGCCGCGCTGCCCTGCCACAGCGCCACGCGCTTCAGACCCCACTGGGAGTCC
CTGGACGCCCGCCAGCTGCCCGCGTGGTTTGACCAGGCCAAGTTCGGCATCTTCATCCACTG
GGGAGTGTTTCCGTGCCAGCTTCGGTAGCGAGTGGTTCTGGTGGTATTGGCAAAAGGAAA
AGATACCGAAGTATGTGGAATTTATGAAAGATAATTACCTCCCTAGTTTCAAATATGAAGAT
TTTGGACCACTATTTACAGCAAAATTTTTTAATGCCAACAGTGGGCAGATATTTTTTCAGGC
CTCTGGTGCCAATACATTGTCTTAACTTCCAAACATCATGAAGGCTTTACCTTGTGGGGGT
CAGAATATTCGTGGAAC TGGAATGCCATAGATGAGGGGCCCAAGAGGGACATTGTCAAGGAA
CTTGAGGTAGCCATTAGGAACAGAAGTACCTGCGCTTTGGACTGTACTATTCCCTTTTGA
ATGTTTTCATCCGCTCTCTCTTGAGGATGAATCCAGTTCATTCCATAAGCGCAATTTCCAG
TTTCTAAGACATTGCCAGAGCTCTATGAGTTAGTGAAACAATATCAGCCTGAGGTTCTGTGG
TCGGATGGTGACGGAGGAGCACCGGATCAATACTGGAACAGCACAGGCTTCTTGGCCCTGGTT
ATATAATGAAAGCCAGTTTCGGGGCA CAGTAGTCACCAATGATCGTTGGGGAGCTGGTAGCA
TCTGTAAGCATGGTGGCTTCTATACCTGCAGTGATCGTTATAACCCAGGACATCTTTTGCCA
CATAAATGGGAAAACATGCATGACAATAGACAACTGTCTGGGGCTATAGGAGGGAAAGCTGG
AATCTCTGACTATCTTCAATTTGAAGAATTTGGTGAAGCAACTTGTAGAGACAGTTTTCATGTG
GAGGAAATCTTTTGATGAATATTTGGGCCACACTAGATGGCACCCATTCTGTAGTTTTTGGAG
GAGCGCATGAGGCAAGTGGGGTCTGGCTAAAAGTCAATGGAGAAGCTATTTTGAACCTTA
TACCTGGCGATCCAGAATGACACTGTCACCCAGATGTGTGGTACACATCCAAGCCTAAAG
AAAAATTAGTCTATGCCATTTTTCTTAAATGGCCCAATCAGGACAGCTGTTCCTTGGCCAT
CCCAAAGCTATTCTGGGGGCAACAGAGGTGAAACTACTGGGCCATGGACAGCCACTTAACTG
GATTTCTTTGGAGCAAAATGGCATTATGGTAGAACTGCCACAGCTAACCATTCATCAGATGC
CGTGTAATGGGGCTGGGCTCTAGCCCTAACTAATGTGATCTAAAGTGCAGCAGAGTGGCTG
ATGCTGCAAGTTATGTCTAAGGCTAGGAACATCAGGTGTCTATAATTGTAGCACATGGAGA
AAGCAATGTAACTGGATAAGAAAAATTATTTGGCAGTTTCAGCCCTTTCCCTTTTCCCACTA
AATTTTCTTAAATTAACCATGTAACCATTTTAACTCTCCAGTGCACTTTGCCATTAAAGTC
TCTTCACATTGATTTGTTTCCATGTGTGACTCAGAGGTGAGAATTTTTTACATTATAGTAG
CAAGGAATTTGGTGGTATTATGGACCGAACTGAAAATTTTATGTTGAAGCCATATCCCCCATG
ATTATATAGTTATGCATCACTTAATATGGGGATATTTCTGGGAAATGCATTGCTAGTCAAT
TTTTTTTGTGCCCAACATCATAGAGTGATTTTACAAATCCTAGATGGCATAGCCTACTACA
CACCTAATGTGTATGGTATAGACTGTTGCTCCTAGGCTACAGACATATACAGCATGTTACTG
AATACTGTAGGCAATAGTAACAGTGGTATTTGTATATCGAAACATATGGAAACATAGAGAAG
GTACAGTAAAAATACTGTAATAATAATGGTGCACTGTATAGGGCACTTACCACGAATGGAG
CTTACAGGACTGGAAGTTGCTCTGGGTGAGTCAGTGAGTGAATTTGAAGGCTTAGGAGCTTA
TTGAACACTGCCAGAGCTTATAAAATACTGTATGCTTAGGCTACACTACATTATAAAAAAA
GTTTTTCTTTCTTCAATTATAAAATAACATAAGGTGACTGTAACTTTACAAACGTTTTAATT
TTTAAACCTTTTGGCTCTTTTGTAAATAACACTTAGCTTAAACATAAACTCATTGTGCA
ATGTA

FIGURE 72

MRPQELPRLAFPLLLLLLLLLPPPPCPAHSATRFDPTWESLDARQLPAWFDQAKFGIFIHWG
VFSVPSFGSEWFWWYQKEKIPKYVEFMKDNYPPSFKYEDFGPLFTAKFFNANQWADIFQAS
GAKYIVLTSKHHEGFTLWGSEYSWNWNAIDEGPKRDIVKELEVAIRNRTDLRFGLYYSLFEW
FHPLFLEDESSSFHKRQFPVSKTLPELYELVNNYQPEVLWSDGDGGAPDQYWNSTGFLAWLY
NESPVRGTVVTNDRWGAGSICKHGGFYTCSDRYNPGHLLPHKWENCMTIDKLSWGYRREAGI
SDYLTIEELVKQLVETVSCGGNLLMNIGPTLDGTISVVFEERLRQVGSWLKVNGEAIYETYT
WRSQNDTVTPDVWYTSKPKKELVYAIFLKWPTSGQLFLGHPKAILGATEVKLLGHGQPLNWI
SLEQNGIMVELPQLTIHQMPCKKWGWALALTNVI

Signal sequence:

amino acids 1-28

N-glycosylation site.

amino acids 171-175, 239-243, 377-381

Casein kinase II phosphorylation site.

amino acids 32-36, 182-186, 209-213, 227-231, 276-280, 315-319,
375-375

Tyrosine kinase phosphorylation site.

amino acids 361-369, 389-397

N-myristoylation site.

amino acids 143-149, 178-184, 255-261, 272-278, 428-434

Leucine zipper pattern.

amino acids 410-432

Alpha-L-fucosidase putative active site.

amino acids 283-295

FIGURE 73

AGCAGGGAAATCCGGATGTCTCGGTTATGAAGTGGAGCAGTGAAGTGTGAGCCTCAACATAGT
TCCAGAACTCTCTCCATCCGGACTAGTTATTGAGCATCTGCCTCTCATATCACCAGTGGCCATC
TGAGGTGTTTCCCTGGCTCTGAAGGGTAGGCACGATGGCCAGGTGCTTACGCTGGTGTG
CTTCTCACTTCCATCTGGACCAAGAGGCTCCTGGTCCAAGGCTCTTTCGGTGCAGAAAGACT
TTCCATCCAGGTGTCTGACAGAAATATGGGGATCACCCCTTGTGAGCAAAAAGGCGAACCCAGC
AGCTGAATTTACAGAACTTAAGGAGGCTGTAGGCTGCTGGGACTAAGTTTGGCCGGCAG
GACCAAGTTGAAACAGCCTTGAAGCTAGCTTTGAACTTGCAGCTATGGCTGGGTGGAGA
TGGATTTCGTGGTCTCTTAGGATTAGCCCAAACCCCAAGTGTGGGAAAAATGGGGTGGGTG
TCCTGATTTGGAAGGTTCCAGTGAGCCGACAGTTTGCAGCTATTTGTTACAACTCATCTGAT
ACTTGGACTAACTCGTGCAATCCAGAAATATCACCACCAAGATCCCATATTCACACTCA
AACTGCAACACAAAACAGAAATTTATTGTCACTGACAGTACCTACTCGGTGGCATCCCTT
ACTCTACAATACCTGCCCTACTACTACTCTCTCTCCAGCTCCAGCTTCCACTTCTATTCCACGG
AGAAAAAATTGATTTGTGTACAGAAAGTTTATGGAACCTAGCACCATGTCTACAGAAAC
TGAACCATTTGTTGAAAATAAAGCAGCATTCAAGAAATGAAGCTGCTGGGTTTGGAGGTGCC
CCACGGCTCTGCTAGTGCTTGTCTCTCTCTTGGTGTGACAGTGGTCTTGGATTTTGC
TATGTCAAAGGTATGTGAAGGCTTCCCTTTTACAAACAAGAAATCAGCAGAAGGAAATGAT
CGAAACCAAAGTAGTAAAGGAGGAGAAAGCCAAATGATAGCAACCCCTAATGAGGAATCAAAGA
AAACTGATAAAAACCCAGAAGAGTCCAAGAGTCCAAGCAAAACTACCGTGCGATGCCTGGAA
GCTGAAGTTTAGATGAGACAGAAATGAGGAGACACCTTGAGGCTGGTTTCTTTCATGCTCC
TTACCTGCGCCAGCTGGGGAAATCAAAGGGCCAAAGAACCAAGAAAGTCCACCTT
GGTCTCTAACTGGAATCAGCTCAGGACTGCCATTTGGACTATGGAAGTGCACCAAGAGAATGC
CCTTCTCCTTATTGTAACCTGTCTGGATCCTATCCTCTACCTCAAAGCTTCCACGGCC
TTTCTAGCCTGGCTATGTCTTAATAATATCCCACTGGGAGAAAGGAGTTTTCGAAAGTGCAA
GGACCTAAAACATCTCATCAGTATCCAGTGGTAAAAAGGCTCCTGGCTGTCTGAGGCTAGG
TGGGTTGAAAGCCAAGGAGTCACTGAGACCAAGGCTTCTCTACTGATTCCGACAGCTCAGAC
CCTTCTCTCAGCTCTGAAAGAGAAACACGTATCCCACTGACATGTCTCTTCTGAGCCCGGTA
AGAGCAAAAGAAATGGCAGAAAAGTTAGCCCTGAAAGCCATGGAGATTCTATAACTTGAG
ACCTAATCTCTGTAAGCTAAAATAAAGAAATAGAACCAAGGCTGAGGATACGACAGTACACT
GTCAGCAGGAGCTGTAAACACAGACAGGGTCAAAGTGTCTCTGAAACACATTGAGTTGGA
ATCACTGTTTAGAACACACACACTTACTTTTCTGGTCTCTACCACTGCTGATATTTCTCT
AGGAAATATACTTTTACAAGTAACAAAAATAAAACTCTTATAAATTTCTATTTTATCTGA
GTTACAGAAATGATTACTAAGGAAGATTACTCAGTAATTTGTTTAAAAAGTAATAAAATTC
ACAAACATTGTGCTGAATAGCTACTATATGTCAAGTGTCTGTCAAGGTATTACACTCTGTAAT
TGAATATTTCTCTCAAAAAATTGACATAGTAGAACGCTATCTGGGAAGCTATTTTCTTCA
GTTTGTATTTCTAGCTTATCTACTTCCAACTAATTTTATTTTGTCTGAGACTAATCTT
ATTCAATTTCTCTAATATGGCAACCATTATAACCTTAATTTATTATTAACTACCTAAGAG
TACATTGTTACCTCTATATACCAAGCACATTTTAAAGTGCCATTAAACAAATGTATCACTA
GCCCTCCTTTTCCAAACAAGGAGGACTGAGAGATGCAGAAATTTTGTGCAAAAAATTA
AGCATTAGAAACTT

00004765-071201

FIGURE 74

MARCFSLVLLLTISIWTRLLVQGSRLAEELSIQVSCRIMGITLVSKKANQQLNFTEAKEACR
LLGLSLAGKDQVETALKASFETCSYGWVGDFVVISRISPNPKCGKNGVGVLWKFVSRQF
AAYCYNSSDTWTNSCIPEIIITTKDPIFNTQTATQTTEFIVSDSTYSVASPYSTIPAPTTTPP
APASTSIPRRKKLICVTEVFMETSTMSTETEPFVENKAAPKNEAAGFGGVPTALLVLALLFF
GAAAGLGFCYVKRYVKAFPFTNKNQQKEMIETKVVKEEKANDSNPNEESKKTDKNPESKSP
SKTTVRCLAEV

Signal sequence:

amino acids 1-16

Transmembrane domain:

amino acids 235-254

N-glycosylation site.

amino acids 53-57, 130-134, 289-293

Casein kinase II phosphorylation site.

amino acids 145-149, 214-218

Tyrosine kinase phosphorylation site.

amino acids 79-88

N-myristoylation site.

amino acids 23-29, 65-71, 234-240, 235-239, 249-255, 253-259

FIGURE 75

AGATGGCGGTCTTGGCACCTCTAATTGCTCTCGTGATTTCGGTGCCGCGACTTTCACGATGG
CTCGCCCAACCTTACTACCTTCTGTGCGCCCTGCTCTCTGCTGCCTTCTACTCGTGAGGAA
ACTGCCCGCGCTCTGCCACGGTCTGCCCACCAACGCGAAGACGGTAACCCGTGTGACTTTG
ACTGGAGAGAAGTGGAGATCTGATGTTTCTCAGTGCCATTGTGATGATGAAGAACCGCAGA
TCCATCACTGTGGAGCAACATATAGGCAACATTTTCATGTTTAGTAAAGTGGCCAACACAAT
TCTTTTCTTCCGCTTGGATATTGCGATGGGCCCTACTTTACATCACACTCTGCATAGTGTTCC
TGATGACGTGCAAACCCCCCTATATATGGGCCCTGAGTATATCAAGTACTTCAATGATAAA
ACCATTGATGAGGAACTAGAACGGGACAAGAGGGTCACCTGGATTGTGGAGTTCCTTGCCAA
TTGGTCTAATGACTGCCAATCATTGCCCCCTATCTATGCTGACCTCTCCCTTAAATACAAC
GTACAGGGCTAAATTTTGGGAAGGTGGATGTTGGACGCTATACTGATGTTAGTACGCGGTAC
AAAGTGAGCACATACCCCTCACCAAGCAACTCCCTACCCTGATCCTGTTCCAAGGTGGCAA
GGAGGCAATGCGCGGCCACAGATTGACAAGAAAGGACGGGCTGTCTCATGGACCTTCTCTG
AGGAGAATGTGATCCGAGAATTTAACTTAAATGAGCTATACCAGCGGGCCAAGAACTATCA
AAGGCTGGAGACAATATCCCTGAGGAGCAGCCTGTGGCTTCAACCCCCACCAAGTGTGAGA
TGGGGAAAAACAAGAAGGATAAATAAGATCCTCACTTTGGCAGTGCTTCCTCTCCTGTCAATT
CCAGGCTCTTTCCATAACCACAAGCCTGAGGCTGCAGCCTTTNATTNATGTTTCCCTTTGG
CTNGACTGNGTGGGGCAGCATGCAGCTTCTGATTTTAAAGAGGCATCTAGGGAATTGTGAG
GCACCTTACAGGAAGGCCTGCCATGCTGTGGCCAACGTTCCTGAGGAGCAAGAAAGAGATC
TCATAGGACGGAGGGGAAATGGTTTCCCTCCAAGCTTGGGTCAGTGTGTTAACTGCTTATC
AGCTATTGAGACATCTCCATGGTTTCTCCATGAACTCTGTGGTTTCATCATTCTTCTTAG
TTGACCTGCACAGCTTGGTTAGACCTAGATTTAACCTAAGGTAAGATGCTGGGTATAGAA
CGCTAAGAAATTTCCCCAAGGACTCTTGCTTCCTTAAGCCCTTCTGGCTTCGTTTATGGTC
TTCATTTAAAGTATAAGCCTAACTTTGTGCTAGTCTTAAGGAGAAACCTTTAACCACAAAG
TTTTTATCATTGAAGACAATATTGAACAACCCCTATTTTGTGGGGATTGAGAAGGGGTGAA
TAGAGGCTTGAGACTTTCCTTTGTGTGGTAGGACTTGGAGGAGAAATCCCTTGACTTTCAC
TAAACCTTGTGACATACTCCCCACCCAGTTGATGGCTTTCCGTAATAAAAAGATTGGGATT
TCCTTTTG

FIGURE 76

MAVLAPLIALVYSVPRLSRWLAQPYLLSALLSAAFLLVKRLPPLCHGLPTQREDGNPCDFD
WREVEILMFLSAIVMMKNRRSITVEQHIGNIFMFSKVANTILFFRLDIRMGLLYITLCIVFL
MTCKPPLYMGPEYIKYFNDKTI DEELERDKRVTWIVEFFANWSNDCQSFAPYADLSLKYN C
TGLNFGKVDVGRYTDVSTRYKVSTSPLTKQLPTLILFQGGKEAMRRPQIDKKGRAVSWTFSE
ENVIREFNLNELYQRAKKLSKAGDNIPEEQPVASTPTTVSDGENKKDK

Signal sequence:

amino acids 1-48

Transmembrane domain:

amino acids 111-125

N-glycosylation site.

amino acids 165-169, 185-189

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 154-158, 265-269

Casein kinase II phosphorylation site.

amino acids 51-55, 145-149, 245-249, 286-290, 288-292

N-myristoylation site.

amino acids 188-194, 225-231

Myb DNA-binding domain repeat signature 1.

amino acids 244-253

1. *Staphylococcus aureus* (10⁸ CFU/ml)
 2. *Staphylococcus aureus* (10⁷ CFU/ml)
 3. *Staphylococcus aureus* (10⁶ CFU/ml)
 4. *Staphylococcus aureus* (10⁵ CFU/ml)
 5. *Staphylococcus aureus* (10⁴ CFU/ml)
 6. *Staphylococcus aureus* (10³ CFU/ml)
 7. *Staphylococcus aureus* (10² CFU/ml)
 8. *Staphylococcus aureus* (10¹ CFU/ml)
 9. *Staphylococcus aureus* (10⁰ CFU/ml)
 10. *Staphylococcus aureus* (10⁻¹ CFU/ml)

[illegible]

FIGURE 78

MGLLLLVPLLLLPGSYGLPFYNGFYYSNSANDQNLGNHGHKDLLNGVKLVVETPEETLFTYQ
GASVILPCRYRYEPALVSPRRVRVKWWKLSENGAPEKDVILVAIGLRHRSFGDYQGRVHLRQD
KEHDVSLEIQDLRLLEDYGRYRCEVIDGLEDESGLVELELRGVVFPYQSPNGRYQFNFHEGQQ
VCAEQAAVVASFQELFRAWEEGLDWCNAGWLQDATVQYPIMLPRQPCGGPGLAPGVRSYGPR
HRRLLHRYDVFCFATALKGRVYYLEHPEKLTLEAREACQEDDATIAKVGQLFAAWKFHGLDR
CDAGWLADGSVRYPVVHHPNCGPPEPGVRSFGFPDQPSRLYGVYCYRQH

Signal sequence:

amino acids 1-17

Casein kinase II phosphorylation site.

amino acids 29-33, 53-57, 111-115, 278-282

Tyrosine kinase phosphorylation site.

amino acids 137-145

N-myristoylation site.

amino acids 36-42, 184-190, 208-214, 237-243, 297-303, 307-313

FIGURE 79

GGAGAGCGGAGCGAAGCTGGATAACAGGGGACCGATGATGTGGCGACCATCAGTTCTGCTGC
TTCTGTTGCTACTGAGGCACGGGGCCAGGGGAAGCCATCCCCAGACGCAGGCCCTCATGGC
CAGGGGAGGGTGCACCAGGCGGCCCCCTGAGCGACGCTCCCCATGATGACGCCCACGGGAA
CTTCCAGTACGACCATGAGGCTTTCTGGGACGGGAAGTGCCAAAGGAATTCGACCAACTCA
CCCCAGAGGAAAGCCAGGCCCGTCTGGGGCGGATCGTGACCGCATGGACCGCGCGGGGGAC
GGCGACGGCTGGGTGTCTGCTGGCCGAGCTTCGCGCGTGCGATCGCGCACACGCAGCAGCGGCA
CATACGGGACTCGGTGAGCGCGGCTGGGACACGTACGACACGGACCGCGACGGCGCTGTGG
GTTGGGAGGAGCTGCGCAACGCCACCTATGGCCACTACGCGCCCGGTGAAGAATTTTCATGAC
GTGGAGGATGCAGAGACCTACAAAAAGATGTGGCTCGGGACGAGCGCGGTTTCGGGTGGC
CGACCAGGATGGGGACTCGATGGCCACTCGAGAGGAGCTGACAGCCTTCTGCAACCCCGAGG
AGTTCCCTCACATGCGGGACATCGTGATTGCTGAAACCTTGGAGGACCTGGACAGAAAAAAA
GATGGCTATGTCCAGGTGGAGGAGTACATCGCGGATCTGTACTCAGCCGAGCCTGGGGAGGA
GGAGCCGGCGTGGGTGCAGACGGAGAGGCAGAGTTCGGGACTTCGGGATCTGAACAAGG
ATGGGCACCTGGATGGGAGTGAGGTGGGCCACTGGGTGCTGCCCCCTGCCAGGACCGAGCC
CTGGTGGAAGCCAACCACTGCTGCACGAGAGCGACACGGACAAGGATGGCGGCTGAGCAA
AGCGGAAATCCTGGGTAATTGGAACATGTTTGTGGGCAGTCAGGCCACCAACTATGGCGAGG
ACCTGACCCGGCACCACGATGAGCTGTGAGCACCGCGCACCTGCCACAGCCTCAGAGGCCCG
CACAATGACCGAGGAGGGGCGCTGTGGTCTGGCCCCCTCCCTGTCCAGGCCCCGAGGAG
GCAGATGCAGTCCAGGCATCCTCCTGCCCCTGGGCTCTCAGGACCCCCCTGGGTGCGCTTC
TGTCCTGTACACCCCCAACCCAGGGAGGGGCTGTCATAGTCCAGAGGATAAGCAATAC
CTATTTCTGACTGAGTCTCCAGCCAGACCCAGGGACCTTGCCCCCAAGCTCAGCTCTAA
GAACCGCCCCAACCCCTCCAGCTCCAAATCTGAGCCTCCACCACATAGACTGAACTCCCTT
GGCCCCAGCCCTCTCCTGCCTGGCTGGCTGGGACACCTCCTCTCTGCCAGGAGCAATAA
AAGCCAGCGCCGGGACCTTGAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA
AAAAAAAAAAAAA

FIGURE 80

MMWRPSVLLLLLLLRHGAQKGKPSPDAGPHGQGRVHQAAPLSDAPHDDAHGNFQYDHEAFLGR
EVAKEFDQLTPESQARLGRIVDRMDRAGDGDGWVSLAELRAWIAHTQQRHIRDSVSAAWDT
YDTRDRDGRVGVWEELRNATYGHYAPGEEFHDVEDAETYYKKMLARDERRFRVADQDGD^{SMATRE}
ELTAFLHPPEEFPHMRDIVIAETLEDLDRNKDGYVQVEEYIADLYSAEPGEEEP^{AWVQTERQQ}
FRDFRDLNKDGHLDGSEVGHVWLPPAQDQPLVEANHLLHESD^{TDKDGRLSKAEILGNWNMFV}
GSQATNYGEDL^{TRHHDEL}

Signal sequence:

amino acids 1-20

N-glycosylation site.

amino acids 140-144

Casein kinase II phosphorylation site.

amino acids 72-76, 98-102, 127-131, 184-188, 208-212, 289-293,
291-295, 298-302

N-myristoylation site.

amino acids 263-269, 311-317

Endoplasmic reticulum targeting sequence.

amino acids 325-330

FIGURE 81

GGGGCCTTGCCTTCCGCACTCGGGCGCAGCCGGGTGGATCTCGAGCAGGTGCGGAGCCCCGG
GCGGCGGGCGCGGGTSCGAGGGGATCCCTGACGCCTCTGTCCCTGTTTCTTTGTCGCTCCAG
CCTGTCTGTCTGTCGTTTGGCGCCCCCGCTCCCGCGGTGCGGGGTGCACACCGATCCTG
GGCTTCGCTCGATTTCGCGCGAGGCGCTCCAGACCTAGAGGGGCGCTGGCCTGGAGCAG
CGGGTCGTCTGTCTCTCTCTCTGCGCGCGCCCGGGGATCCGAAGGGTGGCGGGCTCT
GAGGAGGTGACGCGCGGGGCTCCCGCACCTGGCCTTGCCCGCATTCCTCCCTCTCCTCCAG
GTGTGAGCAGCCTATCAGTCACTATGTCGCGAGCCTGGATCCCGGCTCTCGGCCTCGGTGTG
TGCTGTCTGTCTGCTCCGGGGCCCGCGGGCAGCGAGGGAGCCGCTCCCATTGCTATCACATG
TTTTACAGAGGCTTGGACATCAGGAAAGAGAAAGCAGATGTCCTCTGCCAGGGGGCTGCC
CTCTTGAGGAATTTCTGTGTATGGGAACATAGTATATGCTTCTGTATCGAGCATATGTGGG
GCTGTCTGCCACAGGGGAGTAATCAGCAACTCAGGGGACCTGTACGAGTCTATAGCCTACC
TGGTCGAGAAAACATTCTCAGTAGATGCCAATGGCATCCAGTCTCAAATGCTTCTAGAT
GGTCTGCTTCTTTCACAGTAACATAAGGCAAAAGTAGTACACAGGAGGCCACAGGACAAGCA
GTGTCCACAGCACATCCACCAACAGGTAAACGACTAAAGAAAAACCCGAGAAGAAAACGG
CAATAAAGATTGTAAAGCAGACATTGCATTTCTGATTGATGGAAGCTTTAATATTGGGCAGC
GCCGATTTAATTTACAGAAGAAATTTGTTGGAAGTGGCTCTAATGTTGGGAATTGGAAACA
GAAGGACCACATGTGGGCCTTGTTCAGGCCAGTGAACATCCAAAAATAGAATTTTACTTTGAA
AACTTTTACATCAGCCAAAGATGTTTGTGTTGCCATAAAGGAAGTAGGTTTCAGAGGGGGTA
ATTCCAATACAGGAAAAGCCTTGAAGCATACTGCTCAGAAATTTCTCACGGTAGATGCTGGA
GTAAGAAAAGGATCCCAAAGTGGTGGTGGTATTTATTGATGGTTGGCCTTCTGATGACAT
CGAGGAAGCAGGCATTTGTGGCCAGAGAGTTTGGTGTCAATGTATTTATAGTTTCTGTGGCCA
AGCCTATCCCTGAAGAACTGGGGATGGTTCAGGATGTCACATTTGTTGACAAGGCTGTCTGT
CGGAATAATGGCTTCTTCTCTTACCACATGCCCAACTGGTTTGGCACCACAAAATACGTAA
GCCTCTGTGATCAGAAGCTGTGCACTCATGAACAAATGATGTGCAGCAAGACCTGTTATACT
CAGTGAACATTGCCTTTCTAATTGATGGCTCCAGCAGTGTTGGAGATAGCAATTTCCGCCTC
ATGCTTGAATTTGTTTCCAAACATAGCCAAAGACTTTTGAAATCTCGGACATTTGGTGCCAAAGT
AGCTGCTGTACAGTTTACTTATGATCAGCGCACGGAGTTCACTTCTGACTATAGCACCA
AAGAGAATGTCTAGCTGTCTATCAGAAACATCCGCTATATGAGTGGTGAACAGCTACTGGT
GATGCCATTTCTTCACTGTTAGAAATGTGTTTGGCCCTATAAGGGGAGAGCCCAACCAAGAA
CTTCTAGTAATTTGTACAGATGGGCAGTCTATGATGATGTCCAAGGCCCTGCAGCTGTG
CACATGATGCAGGAATCATTCTCTCTGTGTTGGTGTGGCTTGGGCACCTCTGGATGACCTG
AAAGATATGGCTTCTAAACCGAAGGAGTCTACGCTTTCTTCAAGAGAGTTTACAGGATT
AGAACCAATTGTTTCTGATGTCATCAGAGGCATTTGTAGAGATTTCTAGAAATCCCGCAAT
AATGGTAAACATTTTGCAACTGAAAGAAAAAGTACAAGGGGATCCAGTGTGTAATTTGTATT
CTCATAACTAGTAATGCTTTAGCATACTAGAATCAGATACAAAACATTAAGTATGTCAAC
AGCCATTTAGGCAAAATAAGCACTCCTTTAAAGCCGCTGCCTTCTGGTTACAAATTTACAGTGT
ACTTTGTTAAAAACACTGCTGAGGCTTCATAATCATGGCTCTAGAAACTCAGGAAGAGGA
GATAATGTGGATTAAAAACCTTTAAGAGTTCTAACCATGCCCTACTAAATGTACAGATATGCAAA
TTCCATAGCTCAATAAAGAAATCTGATACTTAGACCAAAAAAAAAA

FIGURE 82

MSAAWIPALGLGVCLLLLPGPAGSEGAAPIAITCFTRGLDIRKEKADVLCPGGCPLLEESVY
GNIVYASVSSICGAAVHRGVISNSGGPVRVYSLPGRENYSSVDANGIQSOMLSRWSASFVTVT
KGKSSTQEATGQAVSTAHPPTGKRLKKTPEKKTGNKDKADIAFLIDGSFNIGQRRFNLQKN
FVGKVALMLGIGTEGPHVGLVQASEHPKIEFYLNFTSAKDVLPFAIKEVGFRRGNSNTGKAL
KHTAQKFFTVDAGVRKGIPKVVVFIDGWPSDDIEEAGIVAREFGVNVFIVSVAKPIPEELG
MVQDVTFVDKAVCRNNGFFSYHMPNWFGTTKYVKPLVQKLCTHEQMMCSKTCYNSVNIAFLI
DGSSSVGDSNFRLMLEFVSNIAKTFEISDIGAKIAAVQFTYDQRTFESFTDYSTKENVLAVI
RNIRYMSGGTATGDAISFTVRNVFGPIRESPNKNFLVIVTDGQSYDDVQGPAAAAHDAGITI
FSVGVAWAPLDDLKDMASKPKESHAFFTREFTGLEPIVSDVIRGICRDFLESQQ

Signal sequence:

amino acids 1-24

N-glycosylation site.

amino acids 100-104, 221-225

Casein kinase II phosphorylation site.

amino acids 102-106, 129-133, 224-228, 316-320, 377-381, 420-424,
425-429, 478-482, 528-532

N-myristoylation site.

amino acids 10-16, 23-29, 81-87, 135-141, 158-164, 205-211,
239-245, 240-246, 261-267, 403-409, 442-448, 443-449

Amidation site.

amino acids 145-149

FIGURE 83

CGCCGCGCTCCCGCACCCGCGGCCGCCACCGCGCGCTCCCGCATCTGCACCCGAGGCC
GGCGGCTCCCGCGGGAGCGAGCAGATCCAGTCCGGGCCGCGAGCGCAACTCGGTCCAGTGC
GGCGGCGGCTCGCGGCGCAGAGCGGAGATGCGAGCGGCTTGGGGCCACCTGCTGTGCCTGC
TGCTGGCGGCGGCGGTCCCCACGGCCCCGCGCCCGCTCCGACGGCGACCTCGGCTCCAGTTC
AAGCCCGGCGCGGCTCTCAGCTACCCGAGGAGGAGGCCACCCTCAATGAGATGTTCCGCGA
GGTTGAGGAATGATGGAGGACACGCGACCAAAATTGCGAGCGCGGTGGAAGAGATGGAGG
CAGAAGAAGCTGCTGCTAAAGCATCATCAGAAGTGAACCTGGCAAACCTTACCTCCAGCTAT
CACAATGAGACCAACACAGACACGAAGGTTGGAAATAATACCATCCATGTGCACCGAGAAAT
TCACAAGATAACCAACAACAGACTGGACAAATGGTCTTTTCAGAGACAGTTATCAGATCTG
TGGGAGACGAAGAAGGCAGAGGAGGCCACGAGTGCATCATCGACGAGGACTGTGGGCCAGC
ATGTACTGCCAGTTTGGCAGCTTCCAGTACACCTGCCAGCATGCCGGGCCAGAGGATGCT
CTGCACCCGGGACAGTGAAGTCTGTGGAGACCAGCTGTGTGTCTGGGGTCACTGCACCAAAA
TGGCCACAGGGGCGAGCAATGGGACCATCTGTGACAACAGAGGGAGTGCACAGCCGGGGCTG
TGCTGTGCCTTCCAGAGAGGCTGCTGTTCCTGTGTGTCACACCCCTGCCCGTGGAGGGCGA
GCTTTGCCATGACCCCGCCAGCCGGCTTCTGGACCTCATCACCTGGGAGCTAGAGCTGATG
GAGCCTTGGACCGATGCCCTTGTGCCAGTGGCCTCCTCTGCCAGCCCCAGAGCACAGCCTG
GTGTATGTGTGCAAGCCGACCTTCGTGGGAGCCGTGACCAAGATGGGGAGATCCTGCTGCC
CAGAGAGGTCCCGATGAGTATGAAGTTGGCAGCTTCATGGAGGAGGTGCGCCAGGAGCTGG
AGGACCTGGAGAGGAGCCTGACTGAAGAGATGGCGCTGGGGGAGCCTGCGGCTGCCGCGCT
GCACTGCTGGGAGGGGAAGAGATTAGATCTGGACCAGGCTGTGGGTAGATGTGCATAAGAA
ATAGCTAATTTATTTCCCGAGGTGTGTGCTTTAGGCGTGGGCTGACAGGCTCTTCCCTACA
TCTTCTTCCAGTAAGTTTCCCTCTGGCTTGACAGCATGAGGTGTTGTGCATTTGTTCCAGC
TCCCCAGGCTGTTCTCCAGGCTTCACAGCTTGGTGCTTGGGAGAGTCAGGCAGGGTTAAAC
TGCAAGAGCAGTTTGCCACCCCTGTCCAGATTATTGGCTGCTTTGCCTCTACAGTTGGCAG
ACAGCCGTTTGTTCATATGGCTTGTATAATTGTTGAGGGGAGGAGATGGAAAACATGTGG
AGTCTCCCTCTGATTGGTTTTGGGGAAATGTGGAGAAGAGTGCCTGCTTTGCAAAACATCAA
CCTGGCAAAAATGCAACAAATGAATTTTCCACGAGTTCCTTCCATGGCGATAGGTAGCTG
TGCTTCAGCTGTTGCAGATGAAATGTTCTGTTCACCCCTGCATTACATGTGTTTATTCATCC
AGCAGTGTGTCTCAGCTCCTACCTCTGTGCCAGGGCAGCATTTTCATATCCAAGATCAATTC
CCTCTCTCAGCACAGCCTGGGGAGGGGGTCATTGTTCTCCTCGTCCATCAGGATCTCAGAG
GCTCAGAGACTCAAGCTGCTTGCCCAAGTCACACAGCTAGTGAAGACCAGAGCAGTTTCAT
CTGGTTGTGACTCTAAGCTCAGTGCTCTCTCCACTACCCACACCAGCCTTGGTGCCACCAA
AAGTGCTCCCCAAAAGGAAGGAGAATGGGATTTTCTTGAGGCATGCACATCGGAATTAAG
GTCAAACTAATTCTCACATCCCTCTAAAAGTAACTACTGTTAGGAACAGCAGTGTCTCAC
AGTGTGGGGCAGCGCTCCTTCTAATGAAGACAATGATATTGACACTGCTCCCTCTTGGCAGT
TGCAATTAGTAACCTTTGAAAGGTATATGACTGAGCGTAGCATACAGGTTAACCTGCAGAAACA
GTACTTAGGTAATTGTAGGGCGAGGATTATAAATGAAATTTGCAAAATCACTTAGCAGCAAC
TGAAGACAATATCAACACAGTGGAGAAAAATCAAACGAGCAGGCGTGTGTGAAACATGGTT
GTAATATGCGACTGCGAACACTGAACCTACGCCACTCCACAATGATGTTTTCAGGTGTCA
TGGACTGTTGCCACCATGTTATTCATCCAGAGTCTCTTAAAGTTTAAAGTTGCAGATGATTGA
TAAGCATGCTTTCTTTGAGTTTTAAATATGTATAAACATAAGTTGCATTTGAAATCAAGC
ATAAATCACTTCACTGCCAAAAAATAAAAAAAAAAAAAAAAAAAAAA

123456789101112131415161718192021222324252627282930313233343536373839404142434445464748495051525354555657585960616263646566676869707172737475767778798081828384858687888990919293949596979899100

FIGURE 84

MQRLGATLLCLLLAAAVPTAPAPAPTATSAPVKPGPALSYPQEEATLNEMFREVEELMEDTQ
HKLRSAVEEMEAEBAKASSEVNLANLPFSYHNETNTDTKVGNNTIHVHREIHKITNNQTG
QMVFSETVITSVGDEEGRRSHECIIDEDCGPSMYCQFASFQYTCQPCRQRMCLCTRDSECCG
DQLCVWGHCTKMATRGSNGTICDNQRDCQPGLCCAFQRGLLFPVCTPLPVEGELCHDFASRL
LDLITWELEPDGALDRCPCASGLLCQPHSHSLVYVCKPTFVGSRDQDGEILLPREVPDEYEV
GSFMEEVRQEELEDLERSLTEEMALGEPAAAAAALLGGEI

Signal sequence:

amino acids 1-19

N-glycosylation site.

amino acids 96-100, 106-110, 121-125, 204-208

Casein kinase II phosphorylation site.

amino acids 46-50, 67-71, 98-102, 135-139, 206-210, 312-316,
327-331

N-myristoylation site.

amino acids 202-208, 217-223

Amidation site.

amino acids 140-144

FIGURE 85

AAGGAGGCTTGGGAGGAAAGAGGTAAGAAAGGTTAGAGAACCCTACCTCACAATCTCTCTGGSGCTCAGAAGGACTCTG
 AAGATAACAATAATTTACGCCCATCTCACTCTCCTTCCCTCCCAAACACACATGTGCATGTACACACACACATAC
 CACACATACACCTTCTCTCTCTCTCACTGAAGACTCACAGTCACTCACTCTGTGAGAGGTATAGAAAAAGGACAC
 TAAAGCCTTAAAGGACAGGCGCTGGCCATTACCTCTGCAGCTCTTTGGGCTTGTGTAGTCAAAAAACATGGAGGGGG
 CCAGGCACGGTGACTCACACCTGTAAATCCAGCACTTTTGGGAGACCGAGGTGAGCAGATCACTTGGGTCAGGAG
 TCTGAGACCACTCTGGCCACATCTGGAGAAACCCCATCTCTACTAAAAATACAAAAATTAGCCAGGAGTGTGTGGC
 AGGTGCTCTTAATCCAGCTCACTCAGGTGGCTGAGCCAGGAGAAATCGCTGAATCCAGGAGCGGAGGATCGAT
 CAGCTGAGTGCACCGCTGCTCACTCCAGCCTGGGTGACAGAAATGAGACTCTGTCTCAAAACAAACAAACACGGGAGGA
 GGGGTAGATCTGCTTCTTCAACCTCTTAACTCTGCACTCTCTTCTCCAGGGCTGGCCCTGATGGGCGCTG
 GCAATGACTGAGCAGGCCCGCCCCAGAGGACAGGGAAGAGGCAATTTGAGGAGGCGCAGAGTGTACGCCCG
 GTGTAGAATGACTGGCCCTGGGAGGGTGTCTCTTGGGCCCTGGCAGGTTGTGACCTTACCCTGCAAAACACA
 AAGAGCAGGACTCCAGACTCTCCTTTGTGAATGGTCCCTGCCCTGCAGCTCCACATAGAGGCTTCTCGTGGCCCC
 ACTCTTGTAGCTTGGGTGGCTGGTGCCTCACTGCCACTGTGCCGTGGTACCCTGGCATGTTCCCTGCCCCCCCTCA
 GTGTGCCCTGCCAGATCCGGCCCTGGTATACGCCCCGCTCGTCTTACCGCGAGGCTACCACTGTGGACTGCAATGA
 CCTATTCCTGACGGCAGTCCCCCGCAGCTCCCGCAGGCACACAGACCTGCTCTTGCAGAGCAACAGCATTTGT
 CGTGTGGACAGGAGTGTGAGCTGAGCTACCTTGGCCAAATCTCAGAGAGCTGGACCTGTCCAGAAACAGCTTTTCGGA
 TGCCCGAGACTGTGATTTCTGAGCCCTGCCCAGCTGCTGAGCCTGCACTGAGGAGGAACAGCTGACCCGGCT
 GGAGGACCAAGCTTTTGCAGGCTGGCCAGCCTACAGGAATCTATCTCAACCAACACAGCTCTACCCGATCGC
 CCCCAGGCTCTTTCTGGCCTCAGCAACTTGTGCGGCTGCACTCAACTCAACCTCTTGAAGGCGATTTGACAG
 CGCTGGTGTGAATGCTGCCCAACTTGGAGATCTCATGATTTGGCGGCAACAGGTAGATGCCATCTGGACAT
 GAACTTCCGGCCCTGGCCAACTTGGCTAGCTGGTGTGATGAGCAGCATGAACCTGGCGGAGATCTCCGATATGC
 CTTGAGGGGGTGCAAAAGCCTGGAGAGCCTCTCTTCTATGACAAACAGCTGGCCGGGTGCCCAGGCGGCGCAT
 GGAACAGGTGCCCGGCTCAAGTTCTAGACTCAACAAGAACCCGCTCCAGCGGCTAGGCGCGGGGACTTTGCG
 CAACATGCTGCACCTTAAAGGAGCTGGGACTGAACAAACATGGAGGAGCTGCTCTCATCGAACAGTTTGGCCCTGCT
 GAACCTCCCCGAGCTGACCAAGCTGACACATCAACAAATAAACCAACCGCTGCTCTATCAACCCCTCCGCTTCA
 CCACCTGCCCCAGATGGAGAGCCTCATGCTCAACAAACAGCTCTCATGTGCTTGCACACAGCAGCGGTGAGTGC
 CCTGCCCAACCTTCCAGGAGGAGTCTCCACGCAACCCCATCCGCTGTGACTGTGCTATCCCTCGCTGGCCCAATGC
 CACGGGCAAGGTGTCCGCTCTCATCGAGCCGCAATCCACCTGTGTGTCGAGAGCTCCGGGCTCTCAGGCGCTCCG
 GGTCTCAGGCTGCCCTTCCGGGAGTGCAGGACCACTGTTTGGCCCTCATCTCCCCACGAGCTTCCCCCAAG
 CTTCCAGTGTAGCCAGTGGAGAGCATGTGTCTGATCTGCCGGGCTGCTGCTCCCCACGAGCTTCCCCCAAG
 GGTCACTCCAGCTGGGCTTGCATGTACACTGCCCATGCCCCATGCAGCAGGAGGTACCGGCTGATCCCCGAGGGGACCT
 GGAGCTCGGAGAGGTGACAGCAGAAAGGCGAGGCTATACCTGTGTGGCCGAGAACCTGTGTGGGGGCTGACAC
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 CAACATTAACCCGCTCTCTCAGGCCACGGAGTACTGGGCTGCTGCAAGTGGCCCTTTGCTGATGCCACACCCA
 GTTGGCTTGTGTATGGSCAGGACCAAGAGGCCACTTCTTGCACAGAGCTTGGGGGATCTGCTCTGGGCTCAT
 TGCCATCTCTGCTCTCGTGTCTTCTCTCTGGCAGCTGGGCTAGCGGCCACCTTGGCGACAGGCCCTCCGCTCCCATCTT
 GTGTGTGGGTGGGAGCGGCTCTCCCTCAGGCTGGGCTTTCTGGGGCTGGAGTGGCCCTTCTGTCTGGGTTGT
 GTCTGCTCCCTCGTCTCGCCCTGGAAATCCAGGGAGGAAGCTGCCAGATCTCCAGAGGGGAGACACTGTTGCC
 ACCATTTGTCTCAAAATCTCTAGCTCAGCCTGTTCTCAGCAGTAGAGAAATCACTAGGACTACTTTTACCAAA
 AGAGAACAGTCTGGGCGCAGATGCCCTCCAGGAAAGGACATGGACCAACGCTGTGAGCGCTGGCAGCTGGGCG
 CAAGACAGTGTGGGCTTTGTGGCCCTGGGGGTGCTTCTGCAGCTTGAAGAAAGTTGGCCCTTACCTCTTAGGGTCA
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FIGURE 86

MRLLVAPLLLAUVAGATATVPVVPWHVPCPPQCACQIRPWYTPRSSYREATTVDCNDLFLTA
VPPALPAGTQTLLQLQNSIVRVDQSELGYLANLTELDLSQNSFSDARDCDFHALPQLLSLHL
EENQLTRLEDHSFAGLASLQELYLNHNQLYRIAPRAFSGLSNLLRLHLNSNLLRAIDSRWFE
MLPNLEILMIGGNKVDAILDMNFRPLANLRSLVLAGMNLREISDYALEGLQSLESLSFYDNQ
LARVPRRALEQVPGLKFLDLNKNPLQRVGPGDFANMLHLKELGLNNMEEVLSIDKFALVNL
ELTKLDITNNPRLSFIHPRAFHHLPQMETMLNNAALHQQTVESLPLNQLQEVGLHGNPIR
CDCVIRWANATGTRVRPIEQSTLCAEPPDLQRLPVREVPFREMTHCLPLISPRSFPPSLQ
VASGESMVLHCRALAEPEPEIYVWTPAGLRRLTPAHAGRRYRVYPEGTLELRRVTAAEAGLYT
CVAQNLVGADTKTVSVVVGRALLQPRDEGGQGLELRVQETHPYHILLWSVWTPPNTVSTNLTW
SSASSLRGQGATALARLPRGTHSYNITRLLQATEYWACLQVAFADAHTQLACVWARTKEATS
CHRALGDRPGLIAILALAVLLLAAGLAHLGTGQPRKGVGGRRPLPPAWAFWGSAPSVRV
SAPLVLPWNPGRKLPKRSSEGETLLPPLSQNS

Signal sequence:

amino acids 1-18

Transmembrane domain:

amino acids 629-648

N-glycosylation site.

amino acids 94-98, 381-385, 555-559, 583-587

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 485-489

Casein kinase II phosphorylation site.

amino acids 46-50, 51-55, 96-100, 104-108, 130-134, 142-146,
243-247, 313-317, 488-492, 700-704

Tyrosine kinase phosphorylation site.

amino acids 532-540

N-myristoylation site.

amino acids 15-21, 493-499, 566-572

Amidation site.

amino acids 470-474, 660-664, 692-696

CACACGACAGGGCGCTGTTTGCAGAGAGTCGAAGAAGTCTCGGACCATCTGGAGGAGGGGGACATTGTGTACCGCCT
 CTATCTGCGCGAGACCATCTCAAGGTGATCAAGTGTATCTCTCTATCTGCTACACCGCTCTACTACGTGCACAAA
 CATCAAGTTTCGACCTGTCAGTCGACCGGTGACATGTAGAGCGCTGACGGGTCACCGCATACCGCTGCGCCACC
 CTTGSGCCACATCTTCAAGATCTCGGCGTCTCTTCATCATCGGCTGTATCATCTTTCACGGCCTCATCTGCACTGTA
 CACACTGTGGTGGATGTCTACGGCGCTCCCTCAAGAAGTATCGGTTTGATCGTCATCGTGAGGAGGAGCCTACAG
 CGACATCCGCGACCTCGAAGACGACTTCGCTCTCATGTGCACTCATATTGACCAATACGACCGCGCTCTACTCTCAA
 CGCGCTTCGCCGCTCTTCTGTGCGAGGTGAGTGAGAACAGCTCGGGCAGCTGAACTTCAACACGAGGTGGAGCGCT
 GGACAAAGCTCCGGGACCGCGCTCACCAAGAACCGCGAGGACAGCTGAGACGTGCACCTTGTTCGTTTCATGTCGAT
 CCTTGCACACTGTGTTGACCTGTGTGGAGCTGGAGTGTCTCAAGCTGGAGCTATCCCGACGTGACCATCCCGCC
 CAGGACTTCGCCAGCTCGCGGCTCAAGGAGCTGTGGCTTATACCAACAGCGGCCAGAGTTGAAGCGCCTCGGCT
 GGCCTCTCTGCGCGAGAACTCTCGGGCGCTGCACATCAAGTTACACGCAATCAGGAGATCCCGCTGTGGATCTTA
 TAGCCTGAAGACACTGGAGAGCTGCACCTGACGCGCACTGTAGCGCGGAGAACCAACCGCTCATCTGTCATCTGCA
 CGGGCTCGCGGAGCTCAAACGCTCAAGGTCTCGGCTCGGCTGAGAGCAACTTAAGCAAGCTGCCACAGCTGTGTCA
 AGATGTGGGCGCTGCACCTGCAAGCTGTCTCATCAACAATGAGGGCAACCAAGCTCATGTCTCTCAAGCGCTCAA
 GAGATGGCGAACTGACTGAGCTGGAGCTGATCGGCTGCAAGCTGGAGCGACTCCCCATCCATCTTCAAGCT
 CCAACAGCTTCGAGGAGATGTAGCTCAAGGACCAACCACTCAAGACACTCAGGAGATCATCAGCTTCCAGCACT
 GACCGCCTCAGCTGCTTGAAGCTGTGGTACCAACCACTCGCTTACATCCCATCAGATCGGCAACTCAACCA
 CTTGGGCGCCTTACTCTGAACCGCAACAAGATCGAAGATCCCCACCGACTTCTTACTTCGCGCGAGCTGCG
 CTACTTGGAGCTTACGCCAACCAACTGACCTTCTCTCGCCAGCTGCGCTCTTCGAGAACCTCGAGAACT
 AGCCATCAGCGGCCAGACCGATCGAGACGCTCCTCTCCGAAGCTCTTTCAGTTCGCGGAAGCTTCGGGCGCTCGACT
 GGGCAACAACGCTGCTGCTGACTGCCCTCCAGGTCGGGCGACTGACCAACTGCAGCGATCGAGCTCGCGGG
 CACCGGCTGGAGTCTGCTGCTTGGAGCTGGCGAGTCCCACTGCTCAAGCGCAGCGGCTTGTGTGGAGAA
 GGAACGTTTCAACACATCCACCCGAGTGAAGGAGCGGCTGTGAGGGGCTGACAGGAGAGCGCTTGAAGCGAG
 GCGGCGCCAGCACAGCAAGCAGGAGCGGCTCGGCACTCTCAGGCGCGGAGAGGGCGAGGCTAGCTTCTCCAG
 AACTCCCGCAGCGCAGGACCGACTCGGCGCTGGGAGGAGCTCGGGGCGCTGTGAGTCAAGGCCACGAGGAGA
 GGACAGTATCTGTGGGCGTGCGCCTTTCTCTCTGAGACTCAGTCCCCAGGGCAAGTGTGTGTGAGGAGAG
 AGCAAGTCTCAAGAGCGAGTATTTGGATATCAGGCTCTCTCTTGAGGCGCACTGTGCCCCAGGGGCTGAG
 CTGCCACGAGAGGCTCTGGGAGCTCATCTTAGTTTCTGGTATTTATTTGTTTCCATCTCCCACTCCTCTATCC
 AGTAACTTTATATCATCTCCAGAAAGTTTCAGGCCACGTGGAAGTGTTCAGGGAAGAGGTGGGCTGCTTTTCCCT
 TTGTCTTATTTAGGAGTTCGCGCGGGCATTTAAACACCACTGCACTTCAGCAGAGTGTCTCGGGCGAAGCAC
 CCATGGAGCGGTTCACCAAGCAGTTCGCGGCTGGGCTTCGCGTTCGCTCAGCGGAGAGCGAGGCGCTCAGCTGGG
 AAGCGAGGCGTGAAGCTTGCCTCTCAGTTTGTGGCAGTTTAGTTTGTGTTTTTTTATTTTAA
 AAAACATTTTTTTTTTAAAAAAAGAGTTTGAATAATGAGCTGGTTTGGGATATTAATAAAAAAAAATTTAAAAAA
 AAAAGACATAACGGCCAGTGGTGGAGTTCAGGAGCGAGGTCGGAGTTCCCTTGAGCAAGCAGGACGAGTAT
 TGAATGTGTTTCTGTTTCTGCTGGGCGAGGTCAGGCTGTCTTCGGAATCTGCTGTGACCTTGTGTCAGGAGT
 CTATTGTGTTTCGGGAGGAGGAGTTTTTTGTTGTTTGTGGTTTTTTGGTTTTCTGTTTCTTCTCTCC
 ATGTGTTCTGGCAGCACTATTCTGAGCGTCTCGGCGAGGAGGAATGTTTGGAGTCTGCCAAGGAGGAGGAG
 ACTCGGTTGCTCAATCCCGGAGAGCGGTCTCTCATCTGCACCTCCCTCTGCTGCTGCCCTGCTCTTCCA
 CGCACAGTGTTAAGGAGCCAGAGGAGCACTTCGCCAGACTTGTGTTCCCTACCTCTCGGGCAGTGGGTGTGT
 CCAAGTCACCGCTTGGCTCCAGGCTGTTCTCATGCACTCTGTCGCACTGTGTCATTAAGAGACGACATTA
 GAGGCTGTGTCGGAAATGGGAGGCTCGCCCTGGGAGGAGCGGCTGTGTTCCAGACCGGTTCCCTCTGGCTGGGC
 CTGGAGTGCACAGCCGACTCGGCACCTGGTGGCTGGAAGCACTTCAGTCTTAGATCATCTCGGCTCCCACTCT
 AGAAGAGGCTCCCGGCTTAGATCAATCACTGAGCACTAAGGCACCTTTAGAGTCTCTGCTTAAATGATATGT
 CCACTCGCTCTGTCGTCATTTGTGTTTCTGGCTCGTGTCACTTGGATATATCTCGAATAATGACACACTG
 CTTCTGACCAACTTAGAACAAAAATCCGTTATGCTGGGTCTGAACCTTGTAGCTCGGTCACAGTATCAATAAA
 CTTATTATACGAAAAAAAAAAA

FIGURE 88

MRQTIKVIKIFILIICYTVYYVHNKFDVDCTVDIESLTGYRTYRCAHPLATLFKILASFYI
SLVIFYGLICMYTLWWMLRRSLKKYSFESIREESSYSDIPDVKNDFAFMLHLIDQYDPLYSK
RFAVFLSEVSENKLRQLNLNNEWTLDKLRQLTKNAQDKLELHLFMLSIGIPDITVFDLVELEV
LKLELIPDVTIPPSIAQLTGLKELWLYHTAAKIEAPALAFLENLRLALHIKFTDIKEIPLWI
YSLKTLEELHLTLGNLSAENNRYIVIDGLRELKRLKVLRLKSNLSKLPQVVTDVGVLQKLSI
NNEGTKLIVLNSLKMANLLELELIRCDLERIPHSIFSLHNLQBIDLDKNNLKTIEETISFQ
HLHRLTCLKWNHIAIYIPIQIGNLTNLERLYLNRNKIEKIPTQLFYCRKRLRYDLSSHNNLT
FLPADIGLLQNLQNLAITANRIETLPPELFPQCRKLRLHLGNNVLQSLPSRVGELTNLTQIE
LRGNRLECLPVELGECPLLKRSGLVVEEDLFNTLPPEVKERLWRADKEQA

Transmembrane domain:

amino acids 51-75 (type II)

N-glycosylation site.

amino acids 262-266, 290-294, 328-332, 396-400, 432-436, 491-495

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 85-89

Casein kinase II phosphorylation site.

amino acids 91-95, 97-101, 177-181, 253-257, 330-334, 364-368,
398-402, 493-497

N-myristoylation site.

amino acids 173-179, 261-267, 395-401, 441-447

FIGURE 89

GCCTGTTGCTGATGCTGCCGTGCGGTACTTGTCAATGGAGCTGGCACTGCGGCCTCTCCCGT
CCCCGCGTGGTTGCTGCTGCTGCCGTGCTGCTGGGCCTGAACGCAGGAGCTGTCATTGACT
GGCCCACAGAGGAGGGCAAGGAAGTATGGGATTATGTGACGGTCCGCAAGGATGCCTACATG
TTCTGGTGGCTCTATTATGCCACCAACTCCTGCAAGAACTTCTCAGAACTGCCCTGGTCAT
GTGGCTTCAGGGCGGTCCAGGCGGTTCTAGCACTGGATTGGAAACTTTGAGGAAATTGGGC
CCCTTGACAGTGATCTCAAACACGAAAAACCCTGGCTCCAGGCTGCCAGTCTCCTATT
GTGGATAATCCCGTGGGCATGCGGTTCAAGTTATGTGAATGGTAGTGGTGCCTATGCCAAGGA
CCTGGCTATGGTGGCTTCAGACATGATGGTTCTCCTGAAGACCTTCTTCAGTTGCCACAAAG
AATTCCAGACAGTTCATTCTACATTTTCTCAGAGTCTCTATGGAGGAAAAATGGCAGCTGGC
ATTGGTCTAGAGCTTTATAAGGCCATTGAGCGAGGGACCATCAAGTGCAACTTTGCGGGGGT
TGCTTGGGTGATTCTCGGATCTCCCTGTTGATTGCGTGCTCTCCTGGGGACCTTACCTGT
ACAGCATGTCTCTCTCAAGACAAAGGTCTGGCAGAGGTGCTAAGGTTGCAGAGCAAGTA
CTGAATGCCGTAAATAAGGGGCTCTACAGAGAGGCCACAGAGCTGTGGGGGAAAGCAGAAAT
GATCATTGAACAGAACACAGATGGGGTGAACCTCTATAACATCTTAATAAAGCACTCCCA
CGTCTACAATGGAGTCGAGTCTAGAATTCAACAGAGCCACCTAGTTTGTCTTTGTCAGCGC
CACGTGAGACACCTACAACGAGATGCCTTAAGCCAGCTCATGAATGGCCCCATCAGAAAGAA
GCTCAAAATTATTCTGAGGATCAATCCTGGGGAGGCCAGGCTACCAACGTCTTTGTGAACA
TGGAGGAGGACTTCATGAAGCCAGTCATTAGCATTGTGGACGAGTTGCTGGAGGCAGGGATC
AACGTGACGGTGTATAATGGACAGCTGGATCTCATCGTAGATACCATGGGTGAGGAGCCTG
GGTGGCGGAACTGAAGTGGCCAGAACTGCCTAAATTCAGTCAGCTGAAGTGAAGGCCCTGT
ACAGTGACCCATAATCTTTGAAACATCTGCTTTTGTCAAGTCCTACAAGAACCTTGCTTTC
TACTGGATTCTGAAAGCTGGTCATATGGTTCCTTCTGACCAAGGGGACATGGCTCTGAAGAT
GATGAGACTGGTGACTCAGCAAGAATAGGATGGATGGGGCTGGAGATGAGCTGGTTTGGCCT
TGGGGCACAGAGCTGAGCTGAGGCCGCTGAAGCTGTAGGAAGCGCCATTCTTCCCTGTATCT
AACTGGGGCTGTGATCAAGAAGGTTCTGACCAGCTTCTGCAGAGGATAAAATCATTTGTCTCT
GGAGGCAATTTGGAAATTATTTCTGCTTCTTAAAAAACCTAAGATTTTTTAAAAAATTGAT
TTGTTTTGATCAAAATAAAGGATGATAATAGATATTAA

FIGURE 90

MELALRRSPVPRWLLLLPLLLGLNAGAVIDWPTEEGKEVWDYVTVRKDAYMFWWLYYATNSC
KNFSELPLVMWLQGGPGGSSTGFGNFEEIGPLDSLKPRKTTWLQAASLLFVDNPFVGTGFSY
VNGSGAYAKDLAMVASDMMVLLKTFFSCHKEFQTVPFYIFSES YGGKMAAGIGLELYKAIQR
GTIKCNFAGVALGDSWISPVDSVLSWGPVLYSMSLLEDKGLAEVSKVAEQVLNAV NKGLYRE
ATELWGKAEMII EQNTDGVNFYNILTKSTPTSTMESSELEFTQSHLVCLCQRHVRHLQRDALS
QLMNGPIRKCLKIIPEDQSWGQATNVFVNMEEDFMKPVISIVDELLEAGINVTVYNGQLDL
IVDTMGQEAWVRKLKWPELPKFSQLKWKALYS DPKSLETSAFVKS YKNLAFYWILKAGHMVP
SDQGDMALKMMRLVTQQE

Signal sequence:

amino acids 1-25

N-glycosylation site.

amino acids 64-68, 126-130, 362-366

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 101-105

Casein kinase II phosphorylation site.

amino acids 204-208, 220-224, 280-284, 284-288, 351-355, 449-453

N-myristoylation site.

amino acids 22-28, 76-82, 79-85, 80-86, 119-125, 169-175,
187-193, 195-201, 331-337, 332-338, 360-366

FIGURE 91

GGCCGCGGGAGAGGAGGCCATGGGCGCGCGGGGCGCTGCTGCTGGCGCTGCTGCTGGCTC
GGGCTGGACTCAGGAAGCCGGAGTCGCAGGAGGCGGCGCGTTATCAGGACCATGCGGCCGA
CGGGTCATCACGTCGCGCATCGTGGGTGGAGAGGACGCCGAACTCGGGCGTTGGCCGTGGCA
GGGGAGCCTGCGCCTGTGGGATTCCACGTATGCGGAGTGAGCCTGCTCAGCCACCGCTGGG
CACTCACGGCGGCGCACTGCTTTGAAACCTATAGTGACCTTAGTGATCCCTCCGGGTGGATG
GTCCAGTTTGCCAGCTGACTTCCATGCCATCCTTCTGGAGCCTGCAGGCCCTACTACACCCG
TTACTTCGTATCGAATATCTATCTGAGCCCTCGCTACCTGGGGAATTACCCCTATGACATTG
CCTTGTTGAAGCTGTCTGCACCTGTCACTTACCTAAACACATCCAGCCCATCTGTCTCCAG
GCCTCCACATTTGAGTTTGAGAACCGGACAGACTGCTGGGTGACTGGCTGGGGGTACATCAA
AGAGGATGAGGCACTGCCATCTCCCCACACCTCCAGGAAGTTCAGGTGCCATCATAAACA
ACTCTATGTGCAACCACCTCTTCTCAAGTACAGTTTCCGCAAGGACATCTTTGGAGACATG
GTTTGTGCTGGCAACGCCCAAGGCGGGAAGGATGCCTGCTTCGGTGACTCAGGTGGACCCCTT
GGCCTGTAAACAAGATGGAATGACTGTGGTATCAGATTGGAGTCGTGAGCTGGGGAGTGGGCTGTG
GTCGGCCCCAATCGGCCCGGTGTCTACACCAATATCAGCCACCACCTTTGAGTGGATCCAGAAG
CTGATGGCCCAGAGTGGCATGTCCCAGCCAGACCCCTCCTGGCCACTACTCTTTTCCCTCT
TCTCTGGGCTCTCCCACTCCTGGGGCCGGTCTTGAGCCTACCTGAGCCCATGCAGCCTGGGGC
CACTGCCAAGTCAGGCCCTGGTTCTTCTGTCTTGTGGTAATAAACACATTCCAGTTGA
TGCCTTGCAGGGCATTTCTCAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

FIGURE 92

MGARGALLALLLARAGLRKPESQEAAPLSGPCGRRVITSRIVGGEDAE LGRWPWQGSRLW
DSHVCVGSLLSHRWALTAAHCFETYSDLSDPGWMVQFGQLTSMPSFWSLQAYYTRYFVSN I
YLSPRYLGNSPYDIALVKLSAPVTTYTKHIQPICLQASTFEFENRTDCWVTGWGYIKEDEALP
SPHTLQEVQVAIINNSMCNHLFLKYSFRKDI FGDMVCAGNAQGGKDACFGDSGGPLACNKNG
LWYQIGVVSWGVGCGRPNRPGVYTNISHHFEW IQKLMAQSGMSQPDPSWPLLFFP LLWALPL
LGPV

Signal sequence:

amino acids 1-18

N-glycosylation site.

amino acids 167-171, 200-204, 273-277

Casein kinase II phosphorylation site.

amino acids 86-90, 134-138, 161-165, 190-194, 291-295

N-myristoylation site.

amino acids 2-8, 44-50, 101-107, 225-231, 229-235, 239-245,
259-265, 269-275

Amidation site.

amino acids 33-37

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 252-263,

Serine proteases, trypsin family, histidine active site.

amino acids 78-84

FIGURE 93

CCCACGCGTCCGCGGACGCGTGGGAAGGGCAGAATGGGACTCCAAGCCTGCCTCTTAGGGCT
CTTTGCCCTCATCCTCTCTGGCAAAATGCAGTTACAGCCCGGAGCCCCAGCAGCGGAGGACGC
TGCCCCCAGGCTGGGTGTCCCTGGGCGCTGCGGACCCTGAGGAAGAGCTGAGTCTCACCTTT
GCCCTGAGACAGCAGAATGTGGAAAGACTCTCGGAGCTGGTGAGGCTGTGTCCGGATCCAG
CTCTCCTCAATACGGAAAAATACCTGACCCTAGAGAATGTGGCTGATCTGGTGAGGCCATCCC
CACTGACCCCTCCACACGGTGC AAAAATGGCTCTTGGCAGCCGGAGCCCCAGAAAGTCCCAATTCT
GTGATCACACAGGACTTTCTGACTTGCTGGCTGAGCATCCGACAAGCAGAGCTGCTGCTCCC
TGGGGCTGAGTTTTCATCACTATGTGGGAGGACCTACGGAACCCATGTTTGAAGTCCCCAC
ATCCCTACCAGCTTCCACAGGCCCTTGCCCCCATGTGGACTTTGTGGGGGGACTGCACCGT
TTTCCCCAACATCATCCCTGAGGCAACGTCCTGAGCCGAGGTGACAGGGACTGTAGGCCT
GCATCTGGGGGTAAACCCCTCTGTGATCCGTAAGCGATACAACCTGACCTCACAAGACGTGG
GCTCTGGCACAGCAATAACAGCCAAGCCTGTGCCAGTTCCCTGGAGCAGTATTTCCATGAC
TCAGACCTGGCTCAGTTCATGCGCCTCTTCGGTGGCAACTTTGCACATCAGGCATCAGTAGC
CCGTGTGGTTGGACAACAGGGCCGGGGCCGGGCGGGATTGAGGCCAGTCTAGATGTGCAGT
ACCTGATGAGTGCTGGTGCCAAACATCTCCACCTGGGTCTACAGTAGCCCTGGCCGGCATGAG
GGACAGGAGCCCTTCTGCAGTGGCTCATGTGCTCAGTAATGAGTCAGCCCTGCCACATGT
GCATACTGTGAGCTATGGAGATGATGAGGACTCCCTCAGCAGCGCCTACATCCAGCGGGTCA
ACACTGAGCTCATGAAGGCTGCCGCTCGGGGTCTCACCCTGCTCTTCGCTCAGGTGACAGT
GGGGCCGGGTGTTGGTCTGTCTCTGGAAAGACACCAAGTTCCGCTCTACCTTCCCTGCCTCAG
CCCCATGTGCACACAGTGGGAGGCACATCCTTCCAGGAACCTTTCATCACAAATGAAA
TTGTTGACTATATCAGTGGTGGTGGCTTCAGCAATGTGTTCCACCGGCTTCATACCAGGAG
GAAGCTGTAAAGAAAGTTCCCTGAGCTCTAGCCCCACCTGCCACCATCCAGTTACTTCAATGC
CAGTGGCCGTGCCCTACCAGATGTGGCTGCACCTTTCTGATGGCTACTGGGTGGTCAGCAACA
GAGTGGCCATTCCATGGGTGTCCGGAACCTCGGCCCTCTACTCCAGTGTTTGGGGGGATCCTA
TCCTTGATCAATGAGCACAGGATCCTTAGTGGCCGCCCTCTTGGCTTTCTCAACCCAG
GCTCTACCAGCAGCATGGGGCAGGTCTCTTTGATGTAACCCGTGGCTGCCATGAGTCTGTGC
TGGATGAAGAGGTAGAGGGCCAGGGTTCTGTCTGCTGCTGCTGGCTGGGATCTCTGTAACAGGC
TGGGAACACCAACTTCCCAGCTTTGCTGAAGACTCTACTCAACCCCTGACCCCTTCCCTATC
AGGAGAGATGGCTTGTCCCTGCCCCTGAAGCTGGCAGTTCTAGTCCCTTATTCGCCCCGTG
GAAGCCCTGCTGAACCCCTCAACTATTGACTGCTGCAGACAGCTTATCTCCCTAACCCCTGAAA
TGCTGTGAGCTTGACTTGACTCCCAACCTACCATGCTCCATCATACTCAGGTCTCCCTACT
CCTGCCTTAGATTCTCAATAAGATGCTGTAACCTAGCAATTTTTGAATGCCTCTCCCTCCG
ATCTCATCTTTCTCTTTTCAATCAGGCTTTTCCAAAGGGTTGTATACAGACTCTGTGCACTA
TTTCACTTGATATTCATTCCTCAATTCAGTGAAGGAGACCTCTACTGTACCCGTTTACTCT
TTCTTACCCTGACATCAGAAACAATGGCCCTCCAGTGCACTACTTCAATCTTTGCTTTATG
GCCTTTCCATCATAGTTGCCCACTCCCTCTCCTTACTAGCTTCCAGGTCTTAACTTCTCTG
ACTACTCTTGTCTCTCTCTCATCAATTTCTGCTTCTTCAATGGAATGCTGACCTTCATTGC
TCCATTGTAGATTTTTGCTCTTCTCAGTTTACTCATTTGCTCCCTGGAAACAAATCACTGACA
TCTACAACCATTACCATCTCACTAAATAAGACTTTCTATCCAATAATGATTGATACCTCAAA
TGTA AAAA

00004765 - 071201

FIGURE 94

MGLQACLLGLFALILSGKCSYSPEPDQRRTLPPGWVSLGRADPEEELSLTFALRQQNVERLS
ELVQAVSDPSSPQYGYKYLLENVADLVRPSPLTLHTVQKWLAAAGAKCHSVITQDFLTCWL
SIRQAELLPLGAEFHHYVGGPTETHVVRSPHPYQLPQALAPHVDFVGGGLHRFPPTSSLRQRP
EPQVTGTVGLHLGVTPSVIRKRYNLTSQDVGSGETSNNSQACAQFLEQYFHDSDLAQFMRLFG
GNFAHQASVARVVGQQGRGRAGIEASLDVQYLSAGANISTWVYSSPGRHEGQEPFLQWLML
LSNESALPHVHTVSYGDDDSLSSAYIQRVNTELMKAARGLTLLFASGDSGAGCWSVSGRH
QFRPTFPASSPYVTTVGGTSFQEPFLITNEIVDYISGGGFSNVFPRPSYQEEAVTKFLSSSP
HLPSSSYFNASGRAYPDVAALSDGYVWVSNRVPIPWVSGTSASTFVFGILSLINEHRILSG
RPPLGFLNPRLYQQHGAGLFDVTRGCHECLDEEVEGQGFCSGPGWDFVTGWGTPTSQLC

Signal sequence:

amino acids 1-16

N-glycosylation site.

amino acids 210-214, 222-226, 286-290, 313-317, 443-447

Glycosaminoglycan attachment site.

amino acids 361-365, 408-412, 538-542

Casein kinase II phosphorylation site.

amino acids 212-216, 324-328, 392-396, 420-424, 525-529

N-myristoylation site.

amino acids 2-8, 107-113, 195-201, 199-205, 217-223, 219-225,
248-254, 270-276, 284-290, 409-415, 410-416, 473-479, 482-488,
521-527, 533-539, 549-555

FIGURE 95

GCCGCGCGCTCTCTCCCGCGCCACACCTGTCTGAGCGGCGCAGCGAGCCGCGGCCCGGGC
GGGTGCTCGGCGCGGAACAGTGTCTCGGCATGCGCAGGGATTCCAGGGCTCCTCTTCTTCTC
TTCTTTCTGCTCTGTGCTGTTGGGCAAGTGAGCCCTTACAGTGCCCCCTGGAAACCACTTG
GCCTGCATACCGCTCCCTGTCTGCTTGTCCCAAGTCTACCTCAATTTAGCCAAGCCAGACT
TTGAGCCGAAGCCAAATTAGAAGTATCTTCTTCATGTGGACCCAGTGTCTAAGGGAAGT
CCACTGCCCACTTACGAAGAGGCCAAGCAATATCTGTCTTATGAAACGCTCTATGCCAATGG
CAGCCGCACAGAGACGCAAGTGGGCATCTACATCCTCAGCAGTAGTGAGATGGGGCCCAAC
ACCGAGACTCAGGGTCTTCAGGAAAGTCTCGAAGGAAGCGGCAGATTTATGGCTATGACAGC
AGGTTCAGCATTTTGGGAAGGACTTCCTGCTCAACTACCTTTCTCAACATCAGTGAAGTT
ATCCACGGGCTGCACCGGCACCTTGGTGGCAGAGAAGCATGTCTCAGAGCTGCCCACTGCA
TACAGTAGGAAAAACCTATGTGAAAGGAACCCAGAAGCTTCGAGTGGGCTTCCTAAAGCCC
AAGTTTAAAGATGGTGGTCGAGGGGCCAACGACTCCACTTCAGCCATGCCCGAGCAGATGAA
ATTTCAAGTGGATCCGGGTGAAACGCACCCATGTGCCCAAGGGTTGGATCAAGGGCAATGCCA
ATGACATCGGCATGGATTATGATTATGCCCTCCTGGAACCTCAAAAAGCCCCACAAGAGAAAA
TTTATGAAGATTGGGGTGAGCCCTCCTGCTAAGCAGCTGCCAGGGGGCAGAATCACTTCTC
TGGTTATGACAAATGACCGACCAGGCAATTTGGTGTATCGCTTCTGTGACGTCAAAGACGAGA
CCTATGACTTGTCTTACCAGCAATGCGATGCCCAGCCAGGGGCCAGCGGGTCTGGGGTCTAT
GTGAGGATGTGGAAGAGACAGCAGCAGAAGTGGGAGCGAAAAATTATTGGCATTTTTTCAGG
GCACCACTGGGTGGACATGAATGGTTCCCCACAGGATTTCAACGTGGCTGTGAGAATCACTC
CTCTCAAATATGCCCAGATTTGCTATTGGATTAAAGGAACTACCTGGATTGTAGGGAGGGG
TGAACAGTGTTCCTCCTGGCAGCAATTAAGGGTCTTCATGTCTTATTTTAGGAGAGGCC
AAATTGTTTTTGTCTATTGGCGTGCACACGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT
CTTATAATCTTTTACCTATTTCTTACAATTGCAAGATGACTGGCTTTACTATTTGAAAACTG
GTTTGTGTATCATATCATATATCATTTAAGCAGTTTGAAGGCATACTTTTGATAGAAAATAA
AAAAAATACTGATTTGGGGCAATGAGGAATATTGACAATTAAGTTAATCTTCACGTTTTTG
CAAACTTGATTTTATTTTCACTCTGAATCTGTTTCAAGATTTATATTAATATTTGGCATA
CAAGAGATATGAAAAAAAAAAAAAAAAA

FIGURE 96

MAGIPGLLFLFLFLLCAVGQVSPYSAPWKPTWPAYRLPVVLPQSTLNLAKPDFGAEAKLEVS
SSCGPQCHKGTPLPTYEEAKQYLSYETLYANGSRTETQVGIIYLSSSGDGAQHRDSGSSGKS
RRKRQIYGYSRFSIFGKDFLLNYPFSTSVKLSTGCTGTLVAEKHVLTAAHCIHDGKTYVKG
TQKL RVGFLKPKFKDGGRGANDSTSAMPEQMKFQWIRVKRTHVPKGWIKGNANDIGMDYDYA
LLELKKPHKRKFMKIGVSPPAKQLPGGRIHFSGYDNDRPGNLVYR FCDVKDETYDLLYQQCD
AQP GASGSGVYVRMWKRQQKWERKIIIGIFSGHQWVDMNGSPQDFNVAVRITPLKYAQICYW
IKGNYLDCREG

Signal sequence:

amino acids 1-19

N-glycosylation site.

amino acids 93-97, 207-211

Glycosaminoglycan attachment site.

amino acids 109-113, 316-320

Casein kinase II phosphorylation site.

amino acids 77-81, 95-99, 108-112, 280-284, 351-355

N-myristoylation site.

amino acids 159-165, 162-168, 202-208, 205-211, 314-320, 338-344

Serine proteases, trypsin family, histidine active site.

amino acids 171-177

FIGURE 97

GCATCGCCCTGGGTCTCTCGAGCCTGCTGCCTGCTCCCCGCCCCACCAGCCA**ATGGT**GTTT
CTGGAGCGCCCCAGCCCTGGGTGGGGGCTGTCTCGGCACCTTCACCTCCCTGCTGCTGCTG
GCGTCGACAGCCATCCTCAATGCGGCCAGGATACCTGTTCCCCCAGCCTGTGGGAAGCCCCA
GCAGCTGAACCGGGTTGTGGGCGGCAGGACAGCACTGACAGCGAGTGGCCCTGGATCGTGA
GCATCCAGAAGAATGGGACCCACCACTGCGCAGGTTCTCTGCTCACCAGCCGCTGGGTGATC
ACTGCTGCCACTGTTTCAAGGACAACCTGAACAAACCATACCTGTTCTCTGTGCTGCTGGG
GGCCTGGCAGCTGGGGAACCCTGGCTCTCGGTCCAGAAAGGTGGGTGTTGCCTGGGTGGAGC
CCCACCTGTGTATTCTTGAAGGAAGTGCCTGTGCAGACATTGCCCTGGTGCCTCTCGAG
CGCTCCATACAGTTCTCAGAGCGGGTCTTGCCTACTGTGCTTCTATCCACCT
CCCTCCAAACACCCACTGCTGGATCTCAGGCTGGGGGAGCATCCAAGATGGAGTTCCCTTGC
CCCACCTCAGACCCTGCAGAAGCTGAAGGTTCTATCATCGACTCGGAAGTCTGCAGCCAT
CTGTACTGGCGGGGAGCAGGACAGGGACCCATCACTGAGGACATGCTGTGTGCGCGCTACTT
GGAGGGGGAGCGGGATGCTTGTCTGGGCGACTCCGGGGGCCCCCTCATGTGCCAGGTGGAGC
GCGCCTGGCTGCTGGCCGCGATCATCAGCTGGGGCGAGGGCTGTGCCGAGCGCAACAGGCCC
GGGGTCTACATCAGCCTCTCTGCGCACCGCTCCTGGGTGGAGAAGATCGTGCAAGGGGTGCA
GCTCCGCGGGCGCGCTCAGGGGGGTGGGGCCCTCAGGGCACCGAGCCAGGGCTCTGGGGCCG
CCGCGCGCTCCT**TAG**GGCGCAGCGGGACGCGGGGCTCGGATCTGAAAGGCGGCCAGATCCACA
TCTGGATCTGGATCTGCGGCGGCCTCGGGCGGTTTTCCCCCGCGTAAATAGGCTCATCTACC
TCTACCTCTGGGGGCCCGACGGCTGCTGCGGAAAGGAAACCCCTCCCCGACCCGCCCGAC
GGCCTCAGGCCCCCTCCAAGGCATCAGGCCCGGCCAACGGCCTCATGTCCCCGCCCCAC
GACTTCGGGCCCCGCCCCGGGCCCCAGCGCTTTTGTGTATATAAATGTTAATGATTTTTAT
AGGTATTGTAAACCTGCCACATATCTTATTTATCTCCAATTTCAATAAATTATTTATT
CTCCAAAAA

FIGURE 98

```
></usr/seqdb2/sst/DNA/Dnaseqs.full/ss.DNA43318
><subunit 1 of 1, 317 aa, 1 stop
><MW: 33732, pI: 7.90, NX(S/T): 1
M V V S G A P P A L G G G C L G T F T S L L L L A S T A I L N A A R I P V P P A C G K P Q Q L N R V V G G E D S T D S E W P
W I V S I Q K N G T H H C A G S L L T S R W V I T A A H C F K D N L N K P Y L F S V L L G A W Q L G N P G S R S Q K V G V A
W V E P H P V Y S W K E G A C A D I A L V R L E R S I Q F S E R V L P I C L P D A S I H L P P N T H C W I S G W G S I Q D G
V P L P H P Q T L Q K L K V P I I D S E V C S H L Y W R G A G Q G P I T E D M L C A G Y L E G E R D A C L G D S G G P L M C
Q V D G A W L L A G I I S W G E G C A E R N R P G V Y I S L S A H R S W V E K I V Q G V Q L R G R A Q G G G A L R A P S Q G
S G A A A R S
```

Signal sequence:

amino acids 1-32

N-glycosylation site.

amino acids 62-66, 96-100, 214-218, 382-386, 409-413, 455-459,
628-632, 669-673, 845-849, 927-931, 939-943, 956-960

Glycosaminoglycan attachment site.

amino acids 826-830

Casein kinase II phosphorylation site.

amino acids 17-21, 39-43, 120-124, 203-207, 254-258, 264-268,
314-318, 323-327, 347-351, 464-468, 548-552, 632-636, 649-653,
671-675, 739-743, 783-787, 803-807, 847-851, 943-947, 958-962,
1013-1017, 1019-1023, 1021-1025

Tyrosine kinase phosphorylation site.

amino acids 607-615

N-myristoylation site.

amino acids 179-185, 197-203, 320-326, 367-373, 453-459, 528-534,
612-618, 623-629, 714-720, 873-879

FIGURE 99

GACGGCTGGCCACCATGCACGGCTCCTGCAGTTCTCTGATGCTTCTGCTGCCGCTACTGCTA
CTGCTGGTGGCCACCACAGGCCCGTTGGAGCCCTCACAGATGAGGAGAAACGTTTGATGGT
GGAGCTGCACAACCTCTACCGGGCCAGGTATCCCCAGCGCCTCAGACATGCTGCACATGA
GATGGGACGAGGAGCTGGCGCCTTCGCCAAGGCCTACGCACGCAGTGCGTGTGGGGCCAC
AACAAGGAGCGCGGGCGCGCGGAGAAATCTGTTCCGCATCACAGACGAGGGCATGGACGT
GCCGCTGGCCATGGAGGAGTGGCACACGAGCGTGAGCTACAACCTCAGCGCCGCCACCT
GCAGCCAGGCCAGATGTGCGGCCACTACACGCAGGTGGTATGGGCCAAGACAGAGAGGATC
GGCTGTGGTTCCCACCTTCTGTGAGAAGCTCCAGGGTGTGAGGAGACCAACATCGAATTACT
GGTGTGCAACTATGAGCCTCCGGGGAACGTGAAGGGGAAACGGCCCTACCAGGAGGGGACTC
CGTGCTCCCAATGTCCCTCTGGCTACCACTGCAAGAACTCCCTCTGTGAACCCATCGGAAGC
CCGGAAGATGCTCAGGATTTCCTTACCTGGTAACGTAGGCCCCATCCTTCGGGCGACTGA
AGCATCAGACTCTAGGAAAAATGGGTACTCCTTCTTCCCTAGCAACGGGGATTCCGGCTTTCT
TGGTAACAGAGGTCTCAGGCTCCCTGGCAACCAAGGCTCTGCCTGCTGTGGAAACCCAGGCC
CCAACITTCCTTAGCAACGAAAGACCCGCCCTCCATGGCAACAGAGGCTCCACCTTGCGTAAC
AACTGAGGTCCCTTCCATTTTGGCAGCTCACAGCCTGCCCTCCTTGGATGAGGAGCCAGTTA
CCTTCCCCAAATCGACCCATGTTCTATCCCCAAATCAGCAGACAAAGTGACAGACAAAAACA
AAAGTGCCCTCTAGGAGCCAGAGAACTCTCTGGACCCCAAGATGTCCCTGACAGGGGCAAG
GGAACCTCTACCCATGCCAGGAGGAGGCTGAGGCTGAGGCTGAGTTGCCCTCCTTCCAGTG
AGGTCTTGCCCTCAGTTTTCAGCCCAGGACAAGCCAGGTGAGCTGCAGGCCACACTGGAC
CACACGGGACACCTCCTCCAAGTCCCTGCCCAATTCCCCAATACCTCTGCCACCGCTAA
TGCCACGGGTGGGCGTGCCCTGGCTCTGCAGTCGTCTTGGCAGGTGACAGGGCCCTGACA
AGCCTAGCGTTGTGTACAGGGCTGAACCTCGGGCCCTGGTCATGTGTGGGGCCCTCTCCTGGGA
CTACTGCTCCTGCCTCCTCTGGTGTGGCTGGAATCTTCTGAATGGGATACCACTCAAAGGG
TGAAGAGGTGAGCTGTCTCCTGTCTCTTCCCCACCCGTGCCCCAGCCCCATAACAAGATA
CTTCTTGGTTAAGGCCCTCCGGAAGGGAAAGGCTACGGGGCATGTGCCCTATCACACCATCC
ATCTGGAGGCACAAGGCCCTGGCTGGCTGCGAGCTCAGGAGGCCGCTGAGGACTGCACACC
GGGCCACACCTCTCCTGCCCTCCCTCCTGAGTCTTGGGGTGGGAGGATTGAGGGAGCT
CACTGCCATACCTGGCCTGGGCTGTCTGCCACACAGCATGTGCGCTCTCCCTGAGTGCCTG
TGTAAGTGGGGATGGGGATTCTTAGGGGCAGATGAAGGACAAGCCCCACTGGAGTGGGGTTC
TTTGAGTGGGGGAGGCAGGGACGAGGGAAGGAAAGTAACCTCTGACTCTCCAATAAAAACTT
GTCCAACCTGTGAAA

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FIGURE 100

MHGSCSFLMLLLPLLLLLVATTGPGVGTDEEKRLMVELHNLRYAQVSP TASDMLHMRWDEE
LAFAKAYARQCVWGHNKERRGENLFAITDEGMDVPLAMEEWHHEREHYNLSAATCSPGQ
MCGHYTQVVWAKTERIGCGSHFCEKLGQVEETNIELLCVNYEPPGNVKGKRPYQEGTPCSQC
PSGYHCKNSLCEPIGSPEDAQDLPLYLVTEAPSF RATEASDSRKMGT PSSSLATGIPAFVLVTEV
SGSLATKALPAVETQAPTSLATKDPPSMATEAPPCVTTEVPSILAAHSLPSLDEEPVTFPKS
THVPIPKSADKVTDKTKVPSRSPENSLDPKMSLTGARELLPHAQEEAEAEELPPSSEVLAS
VFPAQDKPGELQATLDHTGHTSSKSLPNFPNTSATANATGGRALALQSSLPGAEGPDKPSV
SGLNSGPGHVWGP LLGLLLPPLVLGIF

Signal sequence:

amino acids 1-22

N-glycosylation site.

amino acids 114-118, 403-407, 409-413

Glycosaminoglycan attachment site.

amino acids 439-443

Casein kinase II phosphorylation site.

amino acids 29-33, 50-54, 156-160, 195-199, 202-206, 299-303

N-myristoylation site.

amino acids 123-129, 143-149, 152-158, 169-175, 180-186, 231-237,
250-256

Amidation site.

amino acids 82-86, 172-176

Peroxidases proximal heme-ligand signature.

amino acids 287-298

Extracellular proteins SCP/Tpx-1/Ag5/PR-1/Sc7 signature 1.

amino acids 127-138

Extracellular proteins SCP/Tpx-1/Ag5/PR-1/Sc7 signature 2.

amino acids 160-172

FIGURE 101

GTAAC TGAAGTCAGGCTTTTCATTGGGAAGCCCCCTCAACAGAATTTCGGTCATTCTCCAAGTTATG TGTGGACGT
ACTTCGTGTGTTCTCCCTCTGCTTGCTTTTTCACATTAGCAGACCGGACTTAAGTCAACAACAGATTATCTTTTCAT
CAAGGCAAGTTCATGAGCCACTTCAAAGCCTTCGAGAAGTGAAACTGAACCAACAATGAATTGGAGACCAATCC
AAATCTGGGACAGCTCTCGGCCAAATATTACACTTCTCTCTCTGGCTGGGAACAGGATTTGTAATTAACCTCCCTGA
ACATCTGAAAGAGTTTCAGTCCCTTGAAACTTTGGAACCTTAGCAGCAACAATATTTTCAGAGCTCCAAACTGCAAT
TCCAGCCCTACAGCTCAATATCTGTATCTCAACAGCAACCGAGTCACATCAATGGGAACCTGGGTATTTTGACAA
TTTGGCCCAACACACTCCTCTGTGTTTAAAGCTGAAACAGGAACCGAATCTCAGCTATCCCAACCAAGATGTTTAAAT
GCCCCAACTGCAACATCTCGAATTGAACCGAACAAGATTAATAATGTAGATGGACTGACATTTCCAGGCTCTGG
TGCTCTGAAGTCTCTAGAAATGCAAGAAATGGAGTAAACGAAACTTATGGATGGAGCTTTTGGGGCTTGAGCAA
CATGGAAATTTTGACAGTGGCCATTAACAACCTAACAGAGATTACCAAGAGCTGGCTTTACGGCTTGCTGTATGCT
GCAGGAATCTCATCTCAGCCGAATGCCATCAACAGGACTCAGCCCTGATGCCCTGGAGTCTTCGSCAAGAGCTCAG
TGAGCTGGACCTTAACCTTCAATCACTTATCAAGGTTAGATGATTCAGCTTCTCTGGCTTAAGCTTACTTAATAC
ACTGCACATTGGGAACAACAGAGCTCAGCTACATTTGCTGATTGGCTTCCGGGGCTTTTCAGTTTAAAGACTTT
GGATCTGAAGAACAAATGAAATTTCTGGACTATTGAAGACATGAATGGTGTCTTCTCTGGGCTTGACAAACTGAG
CGGACTGATCTCCAAGAAATCGGATCCGTTCTATTACTAAAAAGCTCTCACTGGTTTGGATGCTATGGAGCA
TCTAGACCTGAGTGACAACGCAATCATGTCTTTACAAGGCAATGCATTTTCACAAAATGAAGAAACTGCAACAACT
GCATTTAAATACATCAAGCCTTTTGTGGGACTTGCAGCTAAATGGCTCCCAAGTGGGTGGCGGAAAACAACTT
TCAGAGCTTTGTAAATGCCATTTGTGCCATCTCAGCTTAAATGGCTCCCAAGTGGGTGGCGGAAAACAACTT
TGGCTTTGTGTGTGATGATTTTCCCAAACTCAGATCAGGTTTTCAGGCAGAAACAGCTCGGCAATTAAGAGTTT
CAATTTGATGTTTCACTGCTCAGCTGCCAGCAGTGTATCCCAAGTCTTTTGTGTGGAAAAAGACAAATGA
ACTACTGCATGATGCTGAATGGAAATATTGACACACTCCGGGCCCCAAGTGGGAGGTGATGGAGTATACCA
CATCTCTCGGCTCGCGGGTGGAAATTTGCCAGTGAAGGGAATATCAGTGTGTGATCTTCAATCACTTTTGGTTT
ATCTTACTCTGTGCAAGGCAAGCTTACAGTAAATATGCTTCTCCTCATTACCAAGACGCCCAATGGATCTCACCA
CTCGAGCTGGGGCACTGGCCAGCTTGGAGTGTGCTGTGTGGGGCACCCAGCTCCAGATAGCTTGGCAGAAGGA
TGGGGGCACAGACTCCCGAGCTGCACGGGAGAGACGCAATGCATGTGATGGCCGAGGATGACGTGTCTTTATCTGT
GGATGTGAAGATGAGAGCAATGGGGTATACAGCTGCACAGCTCAGAACAGTGCAGGAAGTATTTACGCAATATGC
AACTCTGACTGTCTTAGAAACACCAATCATTTTTCGGGCCACTGTTGGACCGAACTGTAACTCAAGGGAGAAACAGC
CGTCTCAGTGCATTTGTGGAGGAAGCCCTCCCCCTAACTGAACCTGGAACCAAGATGATAGCCCATTTGTGGT
AACCAGAGAGGCACTTTTTCAGCAGGCAATCAGCTTCTGATTATTGTGGACTCAGATGTCAGTGTATGCTGGGAA
ATACACATGTGAGATGTCTAACCCCTTGGCACTGAGAGAGGAACGTCGCGCTCAGTGTGATCCCCACTCCAACT
CTGCGACTCCCTCAGATGACAGCCCAATCGTTAGACGATGACGGATGGGCCACTGTGGGTGTCTGTATCATAGC
CGTGGTTTGTGTGTGGTGGGCACTGCTGTGTGGTGGTCTATATACACACAGGCGGAGGAATGAAGA
TTGACGACTTACCAACACAGATGAGACCACTTGCAGCAGATATTCCTAGTTATTGTGATCTCAGGGAACGTT
AGCTGACAGGCAAGTGGGTACGTGTCTCAGAAAGTGAAGCCACCAAGCTTTGTGACATCTCAGGTGCTGG
ATTTTTCTTACCAACAATGACAGTGTGGGACCTGCCATATTGACAAATAGCAGTGAAGCTGATGTGAAGCTCAG
CACAGATCTGTTCTTTGTCCGTTTGGGATCCACAGGCCCTATGTTATTGAAGGAAATGTGATGGCTTCG
TCCCTTTTGAAACATATCATACAGTTGCACTCTGACCCAGAAACAGTTTAAATGGACACTATGAGCTCCAGTTA
CATAAAGAAAAAGGAGTCTACCCATGTTCTCATCTTCAGAAAGAACTCTGCGAAGCGAGCTTCAGTAAATATC
GTGGCCTTCAATGTGAGGAAGCTACTTAACTAGTTACTCTCAATAGGAAGCTTGAATGAAATATCTGTG
TCTAAACAAGTCTCTTTAGATTTTATGTCAAATCCAGAGCAGCGTCGGTTGCTCGAGTAACTCTTTCATGGG
TACCTTTGGAAGAGCTCTCAGGAGACCTCACCTAGATGCTTCAAGCTTTGGACAGCCATCAGATGTGCAAGC
AAGAGCCTTTTATTTGAAGCTCATCTTCTCCCAAGCTTGGACTCTGGGTGAGGCAAGATGGGAAGAAAGGAC
AGATTTTCAAGGAAGAAATCAATTTGTACCTTTAAACAGACTTAGAAAACTCAGAGACTCCAAATTTTCAGTC
TTATGACTTGGACACATAGACTGAAATGAGACCAAGGAAAAAGCTTAACATACTACTCTCAAGTGAACCTTTTATTT
AAAGAGAGAAATCTTATGTTTTTTAAATGGAGTTATGAATTTTAAAGGATAAAAATGCTTTTATTTATACAGAT
GAACCAAAATTCATAAAGTTTGAAGAAATTTTATATCTGGGAATGATCTCATATAGAAATACCTTTTAAACTAT
TTTTTTAACTTTGTTTATTGCAAAAGATCTTACGTAAATTAATGATATAAATCATGATTTTATGTATTT
TTATAATGCGAGATTTCTTTTATGAAATGAGTTACTAAAGCATTTTAAATATATACCTGCTGATACCTTTT
TTAAATAGAAGTTACTTCTATTATATTTTGCACATTATATTATAAATAAGTGTCAATTTGAA

FIGURE 102

MVDVLLLSFLCLLPHISRDLNRLSFIKASSMSHLQSLREVKLNNNELETIPNLGPVSAN
ITLLSLAGNRIVEILPEHLKEFQSLSETLDLSSNNISELQTAFFAPLQLKYLNLNSNRVTSMEP
GYFDNLANTLLVLKLNRRNISAIIPKMFKLPLQLHLELNRRNKIKNVGLTFQGLGALKSLKM
QRNGVTKLMDGAFWGLSNMELQLDHNNLTEITKGWLYGLLMLQELHLSQNAINRISPDAWE
FCQKLSELDTFNNHLSRLDDSSFLGLSLNLTLLHIGNNRVSYIADCAFRGLSSLKTLDLKNN
ISWTIEDMNGAFSGDLKRLRLILQGNRIRSITKKAFTGLDALEHLDLSDNAIMSLQGNAFSQ
MKKLQQLHLNLTSSLLCDCQLKWLPPQWVAENNFQSFVNASCAHPQLLKGRSIFAVSPDGFVCD
DFPKPQITVQPETQSAIKGSNLSPICSAASSSDSPMTFAWKDNELLHDAEMENYAHLRAQG
GEVMEYTTILRLREVEFASEGKYQCVISNHFSSSYSVKAKLTVNMLPSFTKTPMDLIRAGA
MARLECAAVGHPAPQIAWQKDGGTDFPAARERRRMHVMPEDDVFFIVDVKIEDIGVYSCTAQN
SAGSISANATLTVLETPSFLRPLLDRTVTKGETAVLQCIAGGSPPKLNWTKDDSPLVVTER
HFFAAGNQLLIIVDSVSDAGKYTCESMNTILGTERGNVRLSVIPTPTCDSPQMTAPSLDDDG
WATVGVVIAIVVCCVVGTSVLVWVVIYHTRRRNEDCSITNTDETNPADIPSYLSSQGTLD
RQDGYVSSSESGSHHQFVTSAGAGFFLPQHDSSGTCCHIDNSSEADVEAATDLFLCPFLGSTGP
MYLKGNYVSGDPFETVHTGCSPPDPTVLMHDHYEPSYIKKKECYPCSHPSEESCERSFSNLSW
PSHVRKLLNTSYSHNEGPGMKNLCLNKSSLDPSANPEPASVASSNSFMGTFGKALRRPHLDA
YSSFGQPSDCQPRAFYLKAHSSPDLDGSGSEEDGKERTDFQEEHNICTFKQTLENYRTPNFQS
YDLDT

Signal sequence:

amino acids 1-19

Transmembrane domain:

amino acids 746-765

N-glycosylation site.

amino acids 62-66, 96-100, 214-220, 382-386, 409-413, 455-459,
628-632, 669-673, 845-849, 927-931, 939-943, 956-960

Glycosaminoglycan attachment site.

amino acids 826-830

Casein kinase II phosphorylation site.

amino acids 17-21, 39-43, 120-124, 203-207, 254-258, 264-268,
314-318, 323-327, 347-351, 464-468, 548-552, 632-636, 649-653,
671-675, 739-743, 783-787, 803-807, 847-851, 943-947, 958-962,
1013-1017, 1019-1023, 1021-1025

Tyrosine kinase phosphorylation site.

amino acids 607-615

N-myristoylation site.

amino acids 179-185, 197-203, 320-326, 367-373, 453-459, 528-534,
612-618, 623-629, 714-720, 873-879

FIGURE 103

GGGGAGAGCAATTGACCATGTAAAGGAGACTTTTTTTTTTGGTGGTGGTGGCTGTGGGTGCCTTGCAAAATG
AAGGATGCAGGACGCGAGCTTTCTCTGGAAACCGAACGCAATGGGATAAACTGATTGTGCAAGAGAGAAAGGAA
GAGCTTTTTCTTGGTGGCCCTGGATCTTAAACACAAATGTGTATATGTGCACACAGGAGCAATTCAGAAATGAAA
TAAACCCAGAGTTAGACCCCGCGGGGGTGTGGTGTGTCTGACATAAATAAATACTTTAAAGCAGCTGTCCCTCTCC
CCACCCCCAAAAAAGGATGATTGGAAATGAAGAACCGAGGATTCACAAAGAAAAAGTATGTTCAATTTTTCTC
TATAAAGGAGAAAGTGAGCCAGGAGATATTTTTGGAATGAAAGTTTGGGGCTTTTTTAGTAAAGTAAAGAACT
GGTGTGGTGGTGTCTTCTTTTTTGAATTTCCCAAGAGGAGAGGAAATTAATAATACATCTGCAAGAGAA
TTTCAGAGAGAAAAAGTTGACCGCGGAGATTTGAGGCAATGATTGGGGGAGAGAAACAGCAGAGCAAGTTGGA
TTTGTGCCTATGTGTACTAAATTTGACGGATTAATTGCAAGTTGGATTTTTCTCATCAACTCCCTTTTTTAAAT
TTTTATCTCCTTTGGTATCAAGATCATGCGTTTTCTCTGTCTTAAACCACTGGATTTCCATCTGGATGTTGCT
GTGATCAGTCTGAAATACAACTGTTTGAATTCAGAAGGACCAACACAGATAAATATGAAATGTTGAAACAAGAT
GACCTTACATCCACAGCAGATAATGATAGGCTCTAGGTTTAAACAGGGCCCTATTGACCCCTCTGTTGGTGTCT
GCTGGCTCTTCAACTTTCTTGGTGGCTGGTCTGGTGGCGGCTCAGACCTGCCCTCTGTGTGCTCCTGCAGCAA
CCAGTTTCAGCAAGGTGATTGTGTTCCGAAAAACCTGCTGAGGTTCCGGATGGCATCTCCACCAACACACCGCT
GCTGAACCTCCATGAGAACCAAAATCCAGATCATCAAAGTGAACAGCTTCAAGCATTTGAGGCATCTGGAATCTCT
ACAGTTGAGTAGGAACCATATCAGAACCATTGAAATTTGGGGCTTTCAATGGTCTGGCGAACCTCAACACTCTGGA
ACTCTTTGACAAATCGCTTACATCCCATCCGAATGGAGCTTTTTGTATACITGTCTAAACTGAAGGACTCTGGTT
GCGAAACACCCCATTTGAAAGCATCCCTCTCTATGCTTTTAAACAGAATTCCTCTTTGCGCGCACTAGACTTAGG
GGAATGAAAGACTTTACATACCTCAGAAAGTGGCTTTGAAAGTCTGTCCAACTTGAGGTATTTGAACTTGC
CATGTGCAACTCCGCGGAAATCCCTTAACCTCACAACGCTCATAAAACTAGATGAGCTGGATCTTTCTGGGAATCA
TTTTATCTGCCATTCAGGACCTGCTCTTTCCAGGTTTGTATGCACCTTCAAAAATCTGGATGATACAGTCCGAGT
TCAAGTGTATGAACCGAATGGCTTTGACCAACCTTCAGTCACTAGTGGAGATCAACCTGGCACCAATAATCTAAC
ATTACTGCTCATGACCTCTTCACTCCCTTGATCATCTAGAGCGGATACATTTACATCAACAACCTTGGAACTG
TAACTGTGACATCTGTGCTCAGCTGGTGTGATTAAGACATGGCCCTCGAACACAGCTGTGTGTCGCGGT
TAACTACTCTCCCAATTTCAAGGGGAGGTACATTTGAGAGCTCGACAGCAATTAATCTACATGCTATGCTCGGT
GATTGTGAGCCCCCTGAGACCTCAATGTCTGAAAGGATGAGCAGCTGAAATGTGCGGGCTCCACATC
CTGACATCTGCTATCTTGGATTACTCCAAATGGAACAGTCATGACATGGGCGTCACAAAGTGGCGGATAGCTGT
GCTCAGTGATGGTACGTTAAATTTTCAAAATGTAACGTGTGCAAGATACAGGCATGTACACATGTATGGTGAGTAA
TTCCGTTGGGAATCTACTGCTTCAGCCACCTGTAATGTACTGTCAGCAACCACTACTCCCTTTCTCTACTTTTC
AACCTGTCAGCTAGAGACTATGGAACCGTCTCAGGATGAGGCAACGACACAGATAAATGTGGGTGCCATCC
AGTGTGCTGCTGGGAGACCAACATGTGACACCTCTCTCACAACACAGAGCAAGGTCGACAGAGAAAACTT
CACCATCCCAGTGACTGATATAACAGTGGGATCCAGGAATTTGATGAGGTCAATGAAGACTACAAAAATCATCAT
TGGGTGTTTGTGGCCATCACACTCATGCTGAGTGTGCTGCTATTTCTCAAGATGAGGAAGCAGCACCA
TCGGCAAAACCATCACGCCCCAACAGGACTGTTGAAATTAATAATGTGGATGATGAGATTACGGGAGACACCC
CATGGAAAGCCACTGCCATGCTGCTATCGAGCATGAGCACCTAAATCACTAATCATACAAATCTCCCTT
CAACCACACAAACAGTTAACACAAATAAATTAATACACAGTTCAAGTCAAGTCAAGCTTATGATCCGAATGAA
CTCAAGAGCAATGTACAAGAGCTCAAACTTAAACATTTACAGAGTTACAAAAAACAAACAAATCAAAAAAAA
GACAGTTTATTAATAAATGACACAAATGACTGGGCTAAATCTACTGTTTCAAAAAAGTGTCTTTCAAAAAAACAA
AAAAAGAAAGAAATTTATTTATTAATAAATTTATTTGGATCTAAAGCAGACAAAAA

FIGURE 104

MLNKMTLHPQQIMIGPRFNALFDPLLVLALLQLLVVAGLVRAQTCPSVCSNQNFSKVIC
VRKNLREVPDGIISTNRLNLHENQIQIIVKNSFKHLRHLLEILQLSRNHIRTIEIGAFNGLA
NLNTLELFDNRLTTIPNGAFVYLSKLELWLRNNPIESIPSYAFNRIPSLRRLDLGELKRLS
YISEGAFEGLSNRLRYNLAMCNLREIPNLTPLIKDELDSLGNHLSAIRPGSFQGLMHLQKL
WMIQSQIQVIERNAFDNLQSLVEINLAHNNLTLLPHDLFTPLHHLERIHLLHNPWNCNDIL
WLSWWIKDMAPSNTACCARCNTPPNLKGRYIGELDQNYFTCYAPVIVEPPADLNVTEGMAAE
LKCRASLTSTSVSWITPNGTVMTHGAYKVRIAVLSDGTLNFTNVTVDQDTGMYTCMVSNSVGN
TTASATLNVTAATTTTFSYFSTVTIVETMEPSQDEARTTDNNVGPTPVVDWETTNTVTTSLTPQ
STRSTEKTFTTIPVTDINSIGIPGIDEVMKTTKIIIGCFVAITLMAAVMLVIFYKMRKQHRQN
HHAPTRTVEIINVDDTEITGDTPMESHLMPAIEHEHLNHYNSYKSPFNHNTTNTVNTINSIHS
VHEPLLIRMNSKDNVQETQI

Signal sequence:

amino acids 1-44

Transmembrane domain:

amino acids 523-543

N-glycosylation site.

amino acids 278-282, 364-368, 390-394, 412-416, 415-419, 434-438,
442-446, 488-492, 606-610

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 183-187

Casein kinase II phosphorylation site.

amino acids 268-272, 417-421, 465-469, 579-583, 620-624

N-myristoylation site.

amino acids 40-46, 73-79, 118-124, 191-197, 228-234, 237-243,
391-397, 422-428, 433-439, 531-537

THE DUNLOP GROUP

ATGAAAGCGCTGCTCAAGCTGCAACTCTGTTGACGTTGGCAGTTTCTTTTCGGTTTCCCTCTCGTCTGTTTGGGGGCA
 TGAAGGCGTTCCGCCCGGGGAGTAAAGAGGAAGTTAGCCGGGACGGCCAGGAGGAGGACGCCGACGCGACCG
 GAGCGCGGCGCTGCACTCTCGGCTGGGAGAGTTTGGCGGGCCGAGCGCGCGCGCTGGGAGCTTCGGGATGCA
 GACTAGGCGCTGCGACCGCTGAGCGGCGCGGACCTCCGTCGCGCGCCGCGGGGTGGGGCTGCTGCTGTGC
 CGGGTCTGGGGGGCTGCTGGCGGCTCCGACAGCGCGCGGCTCGCGGGAACTCGGGGAGCCCTCTGGGGTAGCCGCC
 GAGCGCCCATCGCCCACTACTCGCGCTGCTCGGGGACCTCTGCTGACCTGCAGTCTTAAACCGGCTAGCGCTCTT
 CCAGGACACTCCCGCTCTGGGTGCTCGGCTGCAGCTTAAGTCAACACAGATATCTTACTCAAGGCAAGTCTT
 ATGAGCGCAATCTCAAGAGCTTCGAGAGAGTGAAATCGAAACAAATGAATAGTGAGACACTTCCAAATCTGGGACCA
 GTCTCGCAAAATTTATCACTTCTCTCTTGCTGAAAAGAGGATGTTGAATACTCCCTGAACATCTGAAAGA
 TTTGACTGCCCTTGAACATTTGGACCTTAGACAGTCAACAAATATTCAGAGCTCAAAATGCTATTTCGACCCCTACAG
 TCCAAATATCTGATTTCAACAGCAAGCGAGTCACATCAATGGAACCTGGGTATTTGGAACATTTGGCCAACACA
 CTCTCTTGTTTAAAGCTGAACAGGAACCGACTCTCAGCTATCCCAACCAAGATGTTTAAACTGCCCCCACTGCA
 CATCTCGAATTTGAACCGAAACAAGATTAAGATGTAGATGACTGACATTCAGAGGCTTGGTGCTCTGGAAGTCT
 TCGAAATTCGAAAGAAATGGAGTGAACGAAACTATGGATGGAGCTTTTGGGGGCTGAGCAACTGGAATTTTGG
 CAGCTGACCATAACAACTAACAGAGATTAACAAAGGCTGGCTTTACGCTTGCTGATGCTGACGAAACTTCACT
 CTGACGCAAAATGGCCATCAAGGAGTACGCCCTGATGCTCGGGAGTCTTGCAGGAAGCTCAGTGGAGCTGACATG
 ACTTTCAATCAACTTCAAGGTTAGATGATTAAGCTTCTTGCGCTAGGCTATTAATATCACTGCACTAGTGG
 AACACAGAGTCAGCTACATTGCTGATTTGGCTCTCGGGGGGCTTCCAGTTTAAAGACTTTGGATCTGAGAAGAC
 AATGAAATTTCTTGACTATTTGAAGACATGAATGGTGCTTCTCGGGCTGACAAACTGAGGCGACTGATATCTC
 CAGGAATATTCGATCGGTTCTATTACTAAAAAGCCCTCACTTGTTTGGATGCTTGGAGCATCTAGACTGAGT
 GACAACGCAATCATGCTTTTCAAGGCAATGATTTTCAAAATGAAGAACTGCAACATTCGATTCGATTTAAATACA
 TCAAGCCTTTTGTGCGATTGCGCACTAAAAATGCTCCACAGTGGGTGGCGGAAACACTTTTCAGAGCTTTGTA
 AATGCGAGTTGTGCCATCTCAGCTGCTAAAGGAAGAGCAATTTTGTCTGTAGCCGAGTGGCTTTGTGTTG
 GATGATTTTCCCAAACCCAGATGACAGGTCAGCGTTCAGCGAAACAGCTCGGCAATAAAGGTTTCCAAATTTGAGTTT
 ATCTGCTCAGCTGCGCCAGCAGTGATGATTTCCCAATGACTTTGCTCGCAAAAGAACAAATGAACACTCTGCGATG
 CTGGAATTTGGAATTTGACACACTCTCGGGCCCAAGTGGCGAGTGATGGAGTATACCCACTCTCTCGGCTCT
 CGCGAGTGGAAATTTGGCAGTGAGGGAAATACAGTGTGCTTCTCCAACTCTTTGATCCATCTCACTCTCTGTC
 AAAGCCAGCTTACAGTAATATGCTCTCCCTCATCCACGAAGCCCCATGATCTGACCTCCGATCCGAGCTGGGGCG
 ATGGCACCTTGGAGTGTGCTGCTGTTGGGGCACCCAGCCCCAGATAGCTCTGACGAAGATGGGGGACACAGC
 TTCGAGCTGTCAGCGGAGAGCGCATGTCAGTGTATGCCGAGGATGACGTGTTCTTCTCTGGAATGTGAAGATA
 GAGGACATTTGGGTATACAGCTGTCACAGCTACGAACAGTGCAGGAGATTTTCAGCAAAATGCAACTCTGACTGCTC
 CTGAAACACCATCAATTTTGGCGGCACTTTGGACCGAAGCTGTAACCAAGGGGAAACAGCGTCTCACTAGTGC
 ATTGCTGAGGAGGCCCTCCCTCCAACTGAATTTGACCAACAAGATGATAGGCCATTTGGTGGATTAACGAGAGGCA
 TTTTGTGTCAGCGAGCAATCAGCTCTGATTTATTTGACCTCAGATGTCAGTGTGCTGGGAAATACATGTGGAG
 ATTGCTTAAACACTTTGGCATGAGAGAGGAACTGGGCTCAGTGTGATCCCCACTCAACCGCTGCATCTCCCT
 CAGATGACAGCCCATCTGTTAGACATGACGAGATGAGGAGCGGCGCACTGTGGGTGCTGATCATAGCGCTGTTTGTGTT
 GTGTGGGCAAGCTCATCTGTGTGGTGTGATCATATACACAGAGCGGAGGAATGAAGATTCGACGATTAAC
 AACACAGATGAGCAACTTCCGACAGATATCTCAGTTATTTGTCATTTGTCATTCGAGGAAGCTTAGTCTGACAGGCG
 GAGTGTGACTGCTTCAAGAACTGGAAGCCAGCCACAGTGTGTCATCTTCGAGGAACTGATCTGACAGGCGAG
 CAACCATGACAGTATGGGACCTGCCATATTGACCAATGAGGACAGTGTGAGGAACTGATCTTTCTTCAACA
 TTTGTGTCGTTTGGGATCCACAGGCCCTTATGATTTGAAGGGAATGTGATGTGCTCAGATCTTTTGAACA
 TATCATACAGTGTGACGCTTGACCCAGAGACAGTTTAAATGACACATGACGCGGACTTACATAAAGAAAGAG
 GAGTGTACCCATCTCTCATCTCTCAGAGAAGCTCGGACAGCGGACTTCAAGATATATCTCGTGGCCTTCACAT
 CTGAGGAGGACTATTAACACTAGTTACTTCAACATGAAGGACCTGGAATGAAATATCTGTGCTAAACAGAGTTC
 TCTTAGATTTTAGTGCAAACTCCAGGCGCAGGCTCGGTTGCTCCTGAGTAATCTTTCTAGGCTACCTTTGGAAA
 GCCTCCAGGAGCTCAACTCAGATGCTCTTCAAGCTTTGGACAGCCATCAGATTTGTCAGCCAGAGGCTTTTAT
 TTTGAAGCTCTATTCTTCCCGAGACTTGGACTCTGGGTGACAGGAAGTGGGAAAGAGGACAGATTTTCAGGAA
 GAAATACAACTTTGATCTTTTAAAGACATTTAGAAAACTACAGGATCCAAATTTTCACTCTATGACTTGGAC
 ACATATGACCTGATGAGGACCAAGGAAGCTTAAACTACTCACTCAAGTGAATTTTATTTAAAGAGGAGGAGAT
 CTATTGTTTTTTAAATGGAGTTTGAATTTTAAAGAGTAAATAAGCTTATTTATACAGATGAACCAAAATATAC
 AAAAAGTTATGAAATTTTATATCTGGGAATGAGCTCATATAAGAAATACCTTTTAAACTATTTTAACTTTG
 TTTTATGCAAAAAGTATCTACGTAAATTAATGATATAATCATGATATTTATGATTTTATATGTTATGTTATGCGGAC
 TTTCTTTTATGGAATAAGTATTAACAGATTTTAAATAACTCGCTTGTACCATTTTAAATAGAGATTT
 ACTCTATTATTTTGGACATATATTTATAAATGTGTCAATTTGAAAAAATAAATAAATAAATAAATAAATAAATAA

FIGURE 106

MSAPSLRARAAGLGLLLCAVLGRAGRSDDSGRGELGQPSGVAAERPCPTTCRCLGDLDDCSR
KRLARLPPELPSPWVARLDLHNNRLSFIKASSMSHLQSLREVKNLNNELETIPNLGPFVSANIT
LLSLAGNRIVEILPEHLKEFQSLETLDLSSNNISELQTAFPAQLKLYLYLNSNRVTSMEPGY
FDNLANTLLVLKLNRRNISAIPPKMFKLFPQLQHLELNRRNKIKNVDDGLTFQGLGALKSLKMR
NGVTKLMDGAFWGLSNMEILQLDHNNLTEITKGWLYGLLMLQELHLSQNAINRISPDWAFEC
QKLSLELDLTFNNHLSRLDDSSFLGLSLLNTLHIGNNRVSYIADCAFRGLSSKLTLDLKNNEIS
WTIEDMNGAFSGLDKLRRLIILQGNRIRISITKKAFTGLDALEHLDLSDNAIMSLQGNAFSOMK
KLQQLHLNTSSLLCDQLKWLFPQWVAENNFQSFVNASCAPQLLKGRSIFAVSPDGFVCDFF
PKPQITVQPETQSAIKGNSLSFICSAASSSDSPMTFAWKDKDNEHDAEMENYAHRLAQQGE
VMEYTTILRLREVEFASEGKYQCVISNHFSSSYSVKAKLTVMNMLPSFTKTPMDLTIRAGAMA
RLECAAVGHPAPQIAWQKDGDTDFPAARERRMHVMPEDDVFVIDVKIEDIGVYSCTAQNSA
GSISANATLTVLETPSFLRPLLDRTVTKGETAVLQCIAGGSPPPKLNWTKDDSPLVVTERHF
FAAGNQLLIIVSDSDVSDAGKYTCEMSNTLGTERGNVRLSVIPTPTCDSPQMTAPSLDDDGWA
TVGVVIAVVCVVGTSLVWVVIYHTRRRNEDCSITNTDETNPADIPSYLSSQGLTADRO
DGYVSSSESGSHHQFVTSSGAGFFLPQHDSSGTCCHIDNSSEADVEAATDLFLCPFLGSTGPMY
LKGNVYGSDFPFTYHTGCSDPDRTVLMDHYEPSYIKKKECYPCSHPSSESCERSFSNISWPS
HVRKLNTSYSHNEGPGMKNLCLNKSSLDFFSANPEPASVASSNSFMGTGFKALRRPHLDAYS
SFGQPSDCQPRAFYLKAHSSPDLDGSEEDGKERTDFQEENHICTFKQTLNRYRTPNFQSYDLDT

Signal sequence:

amino acids 1-27

Transmembrane domain:

amino acids 808-828

N-glycosylation site.

amino acids 122-126, 156-160, 274-278, 442-446, 469-473, 515-519,
688-692, 729-733, 905-909, 987-991, 999-1003, 1016-1020

Glycosaminoglycan attachment site.

amino acids 886-890

Casein kinase II phosphorylation site.

amino acids 99-103, 180-184, 263-267, 314-318, 324-328, 374-378,
383-387, 407-411, 524-528, 608-612, 692-696, 709-713, 731-735,
799-803, 843-847, 863-867, 907-911, 1003-1007, 1018-1022,
1073-1077, 1079-1083, 1081-1085

Tyrosine kinase phosphorylation site.

amino acids 667-675

N-myristoylation site.

amino acids 14-20, 36-42, 239-245, 257-263, 380-386, 427-433,
513-519, 588-594, 672-678, 683-687, 774-780, 933-939

Leucine zipper pattern.

amino acids 58-80, 65-87

FIGURE 107

CAAAACCTTGCGTCGCGGAGAGCGCCAGCTTGACTTGAATGGAAGGAGCCCGAGCCCGCGGAGCGCAGCTGAGAC
TGGGGGAGCGCGTTTGGCGCTTGCGGGCGCCGCTCGGCGCGCGGGGCGCAGCAGGGAAGGGGAAGCTGTGGTCTGCC
CTGCTCCACGAGGCGCCACTGGTGTGAACCGGAGAGCCCTGGGTGGTCCGCTCCCTATCCCTCTCTTTATGATA
GAAACCTTTCCACACTGGGAAGGCGAGCGCGAGGCGAGGAGGGCTCATGGTGAGCAAGGAGGCGCGGTGATCTGCAG
GGCACAGCAATTCAGAGTTTACAGATTTTACAGATACCAATGGGAAGGCGAGGAGCGCAAGACAGCTTGCCTGGT
TCCATCAGCCCTTGGCGCCAGGCGCATCTGACTCGGCACCCCTTGCAGGCGACCATGGCCCGAGAGCCGGGTGCTGC
TGCTCCTGTGCTGTGCTGCCGCCACAGCTGCACCTGGGAGCTGTGCTTGCCTGAGGGGCCAGGATTTGGCGCGAA
GTGGCGGCCACAGCCTGAGCCCCGGAAGAGAAGCAATTTGCGGAGGAGGAGCCGGTGTCTGTAATGAGCCCTGAGG
AGCCCGGGGCTTGCCCGCAGCGCGGTGAGTGCCTGCCCGAGAGACTGTGCTGTTCACGAGGCGCTGTGGAGCTGTG
GCGGTATTGACTTGGCTGAGTTCGCGGGGAGCTGCTGAGCACACCAACCTATCTCTGCAGAAACCAACCTG
TGGAAAAGATCTTACCTGTAGGAGCTCTCCCGGCTGCACCGGCTGGAGACACTGAACCTGCAAAACCAACCGCTG
CTTCCCGAGGGCTCCAGAGAAAGCGTTTGAAGCATCTGACCAACCTCAATTACCTGTACTTGGCCAAATAACAAGC
TGACCTTGGCACCCCGCTTCTGCCAAACGCCCTGATCAGTGTGGACTTTGCTGCCAACTATCTCAACAGATCT
ATGGGCTCACCTTTGGCCAGAAGCCAACTTGAGGTCTGTGTACCTGCACAAACCAAGCTGCGAGAGCGCGGGC
TGCCGGACAACATGTTCAACGGCTCCAGCAACGTGAGGTCTCTATCTCTGTCAGCAACTCTGCTGCGCCACGTG
CCAAGCACCTGCGCGCTGCCCTGTACAAGCTGCACCTCAAGAACCAACAGCTGGAGAAGATCCCCCGGGGGCT
TCAGCGAGCTGAGCAGCTGCGGAGCTATACCTGCAGAACCACTACCTGACTGACGAGGGCTGGACAACGAG
CCTTCTGGAAGCTCTCCAGCTGGAGTACCTGGATCTGTCCAGCAACCACTGCTCTCGGGTCCAGCTGGGCTGC
CGCGCAGCTTGGTGTGCTGCTGCACTTGGAGAAGAACGCCATCCGAGCGTGGACGGAATGTGCTGACCCCATCC
GCAGCTGGAGTACCTGTGCTGCACAGCAACCAAGCTGCGGGAGCAGGGCATCCACCAATGGCTTCTCAGGGCC
TCAAGCGGTTGACACGGTGACCTGTACAAACACCGCTGGAGCGCTGCCAGTGGCTGCTGCGCGGTGATG
GCACCTCATGATCTGCACAAACAGATCACAGGCATTGGCCGCGAGGACTTTGCCACCACTACTCTTCTGGAGG
AGCTCAACCTCAGCTACCAACCGCATCACAGCCACAGGTGCACCGCGAGCGCTTCCGCAAGCTGCGGCTCTGTC
GCTCGCTGGAGCTTGTGCGGCAACCGGCTGCACACGCTGCCACTGGGCTGCTCGAAATGTCTATGTCTGAAGG
CCAGCAACCACTGCGCAGCGCCCTGGCCAGCGGGCGCTGCGGGCATGGCTCAGCTGCGTGAGCTGTACTTCA
CCAGCGGAATCAGCTCACAGAGATCCCCGAGGGGCTCCCCGAGTCACTTGAGTACCTGTACTCTGCACAAACA
AGATTATGTGCGTGCCTGCGGCAATGCTTCGACTCCAGCCCACTCAAGGGATCTTTCTCAGGTTTAAACAAGC
TGGCTGTGGGCTCGGTGTGGAGAGTGCCTTCCGAGGGCTGAAGCACTTGCAGGTCTTTGGACAATTGAAGGCACT
TAGAGTTTGGTGACATTTCCAAGGACCGTGGCGCTTGGGGAAGGAAAGGAGGAGGAGGAGGAGGAGGAGG
AGGAAGAGGAAACAAGATAGTGAACAGGTGATGCAGATGTGACCTAGGATGATGGACGCGCGGACTCTTTTCTGC
AGCACAGCTCTGTGCTGTGAGCCCCCACTCTGCGGTGCTCACACAGACACCCAGCTGCACATGAGGCA
TCCACATGACACGGGCTGACACAGTCTCATATCCCCACCCCTTCCACGGCGTGTCCACGGCCAGACATG
ACACACATCACACCCTCAAAACAACAGCTCAGCCACACACAACTACCTTCAAAACCAACAGCTCTGTGTACAC
CCCCACTACCGCTGCACCGCCCTTGAATCATGCAGGGAAGGGTCTGCCCTGCCCTGGCACACACAGGCAACCA
TTCCTCCCCCTGCTGACATGTGTATGCGTATGCATACACACACACACACATGCACATGATGTGCGAA
CAGCCCTCCAAAGCTATGCCACAGACAGCTCTTGCCTCCAGCCAGAATCAGCCATAGCAGCTCGCCGTCTGCCT
GTCCATCTGTCCGTCCGTGCGGAGAGACACAAGGATCCATGCTCTGCTGAGGCGAGTGCCTGACACCCT
GGAATCAACAAAGCTGGCTTTTATTCCTTCCATCTCTATGGGAGCAGGAGCTTCAAGGATGTGCTGGCTGGCC
TGGCCACCCCTCTCCAGGTGCTGGGCAGTCACTCTGCTAAGAGTCCGCTGCACGCGCTGGCAGGCA
CAGGCACTTTCCAATTGGGCAAGCCCACTGGAGGAGGATGGGAGAGCCCCCTGGGTGCTGCTGGGGCTTGGG
CAGGAGTGAAGCAGGCTGATGGGGCTGGGCTGAGCCAGGAGGAGGAGGAGCCAGCTGCACCTAGGAGACCTT
GTTCTTCAGGCTGTGGGGAGGTTCCGGGTGCTTTATTTTATTTCTTTCTAAGGAAAAAATGATAAAAT
CTCAAGCTGATTTTCTGTATAGAAAACTAATATAAAGCACTATCCCTATCCCTGCAAAAAA

FIGURE 108

MEGEEAEQPAWFHQPWRFPGASDSAPPAGTMAQSRVLLLLLLPPQLHLGPFVLAVRAPGFGRS
GGHSLSPREENEFAEEEPVLVLSPEEPGPGPAAVSCPRDCACSQEGVVDCCGGIDLREFPGDLP
EHTNHLSLQNNQLEKIYPEELSRHLRLETNLQNNRLTSRGLPEKAFEHLTNLNYLYLANNK
LTLAPRFLPNALISVDFAANYLTKEYGLTFGQKPNLRSVYLHNNKLADAGLPDNMFGSSNV
EVLILSSNFLRHVPKHLPPALYKLHLKNNKLEKIPPGAFSELSSIRELYLQNNYLTDEGLDN
ETFWKLSSLEYLDLSSNNLSRVPAGLPRSLVLLHLEKNAIRSVDANVLTPIRSLEYLLHSN
QLREQGIHPLAFQGLKRLHTVHLYNNALERVPSGLPRRVRTLMILHNQITGIGREDFATTYP
LEELNLSYNRITSPQVHRDAFRKRLRLSLDLSGNRLHTLPPGLPRNVHVLKVKRNELAALA
RGALAGMAQLRELYLTSNRRLSRALGPRAWVDLAHLQLLDIAGNLTEIPEGLPESLEYLYL
QNNKISAVPANAFDSTPNLKIGIFLRFNKLAVGSVVDSAFRRLKHLQVLDIEGNLEFGDISK
RGRLGKEKEEEEEEEEEETR

Signal sequence:

amino acids 1-48

N-glycosylation site.

amino acids 243-247, 310-314, 328-332, 439-443

Casein kinase II phosphorylation site.

amino acids 68-72, 84-88, 246-250, 292-296, 317-321, 591-595

N-myristoylation site.

amino acids 19-25, 107-113, 213-219, 217-223, 236-242, 335-341,
477-483, 498-502, 539-545, 548-554

Leucine zipper pattern.

amino acids 116-138, 251-273, 258-280, 322-344, 464-486, 471-493,
535-557

FIGURE 109

GGGAGGGGGCTCCGGGCGCGCGCAGCAGACCTGCTCCGGCCGCGCGCCTCGCCGTGTCTCTCGGGAGCGGCAG
 CAGTAGCCCGCGCGCGCGAGGCTGGGGGTTCCTCGAGACTCTCAGAGGGGGCGCTCCCATCGGCGCCACCAACCC
 CAACCTGTTCTCTCGCGCGCCACTGCGCTGCGCGCCAGGACCCGCTGCCAACA**TGGATT**TTTCTCTCGCGCTGGT
 GCTGGTATTCCTCGCTCTACCTGCGAGGCGCGCGCGAGTTTCGACGGGAGGTTGGCCACAGGCAAAATAGTGTATCGAT
 TGCCCTATGTGTGTTTGGTGGGAGGATGACTGCTGCTGGGGCTGGGCTTGAAGCACAGGTGCATGAACACTTA
 TGTGTGCGCAACACGATGCAAACTAGTGAATGTATCGGGCGAAACAAGTGCAAGTGTCAATCTCGTGTATGTCTGG
 AAAAACCTGTTAAATCAAGATCTAAATGAGTGTGGCCTGAAGCCCGCGCCCTGTAAGCACAGGTGCATGAACACTTA
 CGCGAGCTTACAGTGTCTACTGTCTCAACGGATATATGCTCATGCGCGGATGGTTCCTGCTCAAGTGCCTGACCTG
 CTCCTATGCGAAACTGTGAGTATGCTGTGATGTTGTTAAAGGACAAATACGGTGCCAGTGCCCATCCCTGGGCT
 GCACCTGGCTCCTGATGGGAGGACCTGTGTAGATGTTGATGAATGTGCTACAGGAAGAGCCCTCTCGCTCATGATT
 TAGGCAATGTGTCAACACTTTGGGAGCTACATCTGCAAGTGTCTAAAGGCTTCGATCTCATGTATTTGGAGG
 CAAATATCAATGTATGACATAGACGAATGCTCACTTGGTCAGTATCAGTGCAGCAGCTTTGCTCGATGTTATAA
 CGTACGTGGTCCACAAGTGCAGAAATGTAAGAAGGATACAGGGGTGATGGACTGACTTGTGTGTATATCCCAAA
 AGTTATGATTGAACCTTCAGGTCCAATTCATGTACCAAGGGAATGTTACCATTTAAAGGGTGACACAGGAAA
 TAATATTTGGATTTCCTGATGTTGGAAGTACTTGGTGGCTCCGGAAGACACCATATATTCCTCTCATTCATTACCAA
 CAGGCTACTTCTAAGCCAAACAAAGAGCTACACCAAGCCCAACACCAATTCCTACTCCACCAACACCAACCC
 CCTGCCAACAGAGCTCAGAACACCTCTACCACTTACCAACCCAGAAAGGCCAACCCGGACTGACAACTATAGC
 ACCAGCTGCCAGTACACCTCCAGGAGGGATTAAGTGTGACCAACAGGGTACAGACAGACCCCTCAGAAACCCAGAGG
 AGATGTGTTCAAGTGTTCGGTACACAGTTGTAATTTTGACCATGGACTTTGTGGATGGATCAGGAGGAAAGACAA
 TGACTTGCAGTGGGAACCAATCAGGAGCCAGCAGGTTGAACAATATCTGACAGTGTGCGCAGCCAAAGCCCGAGG
 GGGAAAAGCTGCACGCTGGTGTCTACTCTCGCGCCCTCATGCTCCTCAGGAGCCTGTGCTGTCAITCAGGCA
 CAAGTGTACGCGGGCTGCATCTGCGCACCTCCAGTGTGTTGTGAGAAAAACAGGTGCCCGGAGCAGCCCTGTG
 GGGAGAATAATGGTGGCACTGCTGGCTGGAGCAAAACACAGATCACTTGGCAGGGGCTGACATCAAGAGCGAATACA
 AAGATGA**T**TTAAAGGGTTGAAAAAAAGACTCTATGATGAAAAATTAAGGAACTGGGATTATTGAGCTGGAGAAG
 AGAAGACTGAGGCGCAACCAATTTGATGGTTTCAAGTATATGAAAGGTTGGCAGAGAGAGGGTGGCGACAGCTG
 TTCTCCATATGCTCAAGAATAGAACCAAGAGGAACTGGCTTAGACTAGAGTAAAGGAGCATTTCTTGGCAGG
 GCGCATTTTGAAGATCTTCAATAAAAGAGTGTGTTTACCCAGGAAAAAGTAAACAAATATAGAATTTCCCAA
 TAAAAATTTGCTATTATTAAGATGGTTAAAGATGTTCTTACCCAGGAAAAAGTAAACAAATATAGAATTTCCCAA
 AGATGTTTGTATCTACTAGTAGTATGACAGTGAAAACTTTTGAAGTAAATATTTGGACAGGCTTAAATTTAGG
 CATTTCCTCTTGACCTCTCAATGAGAGGGATTGAAAGGGGAAGAGCCACCAATGCTGAGCTCACTGAAATA
 TCTCTCCCTTATGCAATCTTAGCAGTATTAAGAAAAAAGGAACTATTATTCCAAATGAGAGTATGATGGAC
 AGATATTTTAGTATCTCAATGATGTTCTCAGATTTTCTTTTAAAGAGATCTTCAAGGAACACAGTTGAGAGC
 TTTCAATTTGTTCAATGGATGATGTTTCTCAGATTTTCTTTTAAAGAGATCTTCAAGGAACACAGTTGAGAGC
 AGAACAGTAAATATTTTGAACAAATAGGTACAATAGAAGTCTTCTGTCAATTAACCTGGTAAAGAGCAGGCTG
 AGGGGAAAAATAAATCAATAGGCTTTGAGTAACGCGAGAATATAGGCTGTAGATCCATTTTAAATGGTTTCAAT
 TCCTTTATGTCATATACTGCACAGCTGAAGATGAAGGGGAAAAATAAATGAATTTTCAATTCGATGCCAA
 TGATACATTTGCACTAACTAGTGAAGAAGTTATCCAAAGTACTGTATAACATCTGTTTATTATTATGTTTT
 CTAAAAATAAAAGTATGTTGTTTCCAAATGGCCCTAATAAAAAACAATATTGTAATAAAAAACACTGTTAGTAAT

1000
 900
 800
 700
 600
 500
 400
 300
 200
 100
 0

FIGURE 110

MDFLALVLVSSSLYLQAAAEFDGRWPRQIVSSIGLCRYGGRIDCCGWARQSWGQCQPVCQP
RCKHGEICIGPNKCKCHPGYAGKTCNQDLNECGLKPRPCKHRCMNTYGSYKCYCLNGYMLMPD
GSCSSALTCSMANCQYGCDDVVKGQIRCCQCPSPGLHLAPDGRTCDVDDECATGRASCPRFRQC
VNTFGSYICKCHKGFEDLMYIGGKYQCHDIDECSLGQYQCSSFARCYNVRGSYKCKCKEGYQG
DGLTCVYIPKVMIEPSGPIHVPKNGTILKGDGTGNNNWIPDVGSTWWPKTPYIPPIITNRP
TSKPTRTRTPKPTPIPTPPPPPLPTELRTPLPPTTPERPTTGLTTIAPAASTPPGGITVDN
RVQTDPPQKPRGDFVSVLVHSCNFDHGLCGWIREKNDLHWEPIRDPAGGOYLTVSAAKAPGG
KAARLVLPGLRLMHSGLCLSFHVKVTGLHSGTLQVFVRKHGAHGAALWGRNGGHGWRQTQI
TLRGADIKSESQR

Signal sequence:

amino acids 1-17

N-glycosylation site.

amino acids 273-277

Casein kinase II phosphorylation site.

amino acids 166-170, 345-349

Tyrosine kinase phosphorylation site.

amino acids 199-206

N-myristoylation site.

amino acids 109-115, 125-131, 147-153, 191-197, 221-227, 236-242,
421-427, 433-439, 462-468, 476-482

Aspartic acid and asparagine hydroxylation site.

amino acids 104-116, 186-198, 231-243

Cell attachment sequence.

amino acids 382-385

EGF-like domain cysteine pattern signature.

amino acids 75-87

FIGURE 111

CTTCTTTGAAAAGGATTATCACCTGATCAGGTTCTCTCTGCATTGCCCCCTTATGATTGTGA
AATGTGGGCTCAAGGTTCTTCACAACTTTTCCTTTTCCTTTGCAACAGGTGCTTGCTCGGGGCTGA
AGGTGACAGTGCCATCACACACTGTCCATGGCGTCAGAGGTCAGGCCCTCTACCTACCCGTC
CACTATGGCTTCCACACTCCAGCATCAGACATCCAGATCATATGGCTATTTGAGAGACCCCCA
CACAAATGCCAAATACTTACTGGGCTCTGTGAATAAGTCTGTGGTTCCTGACTTGGAAATACC
AACACAAGTTCACCATGATGCCACCCAAATGCATCTCTGCTTATCAACCCACTGCAGTTCCTT
GATGAAGCAATTACATCGTGAAGGTCAACATTGAGGAAATGGAATCTATCTGCCAGTCA
GAAGATACAAGTCACGGTTGATGATCCTGTGCACAAAGCCAGTGGTGCAGATTATCCTCCTCT
CTGGGGCTGTGGAGTATGTGGGGAAACATGACCTTGACATGCCATGTGGAAGGGGGCACTCGG
CTAGCTTACCAATGGCTAAAAAATGGGAGACCTGTCCACACCAGCTCCACCTACTCCTTTTC
TCCCCAAAACAATACCTTTCATATGTCTCCAGTAACCAAGGAAGACATTGGGAATTACAGCT
GCCTGGTGAGGAACCTGTCTCAGTGAAATGGAAAGTGATATCATTATGCCCATCATATATTAT
GGACCTTATGGACTTCAAGTGAATTCTGATAAAGGGCTAAAAGTAGGGGAAGTGTTTACTGT
TGACCTTGGAGAGGCCATCCTATTTGATTGTTCTGCTGATTCTCATCCCCCAACACCTACT
CCTGGATTAGGAGGACTGACAATACTACATATATCATTAAAGCATGGGCCTCGCTTAGAAGTT
GCATCTGAGAAAGTAGCCCAGAAGACAATGGACTATGTGTGCTGTGCTTACAACACATAAC
CGGCAGGCAAGATGAAACTCATTTTCACAGTTATCATCACTCCGTAGGACTGGAGAAGCTTG
CACAGAAAGGAAAAATCATTGTCACTTTTAGCAAGTATACTGGAATATCACTATTTTGTGATT
ATATCCATGTGTCTTCTCTTCCCTATGGAAAAAATATCAACCTTACAAGTTATAAAACAGAA
ACTAGAAGGCCAGGCCAGAAACAGAATACAGGAAAGCTCAAAACATTTTCAGGCCATGAAGATG
CTCTGGATGACTTCGGAATATATGAATTTGTTGCTTTTCAGATGTTTCTGTGTGTTTCCAGG
ATTCCAAGCAGGTCTGTTCCAGCCTCTGATTGTGTATCGGGGCAAGATTTGCACAGTACAGT
GTATGAAGTTATTTCAGCACATCCCTGCCAGCAGCAAGACCATCCAGAGTGAACTTTTCATGG
GCTAAACAGTACATTTCGAGTGAAATTCTGAAGAAACATTTTAAGGAAAAACAGTGGAAGAGT
ATATTAATCTGGAATCAGTGAAGAAACCAGGACCAACCTTTACTCATTATTCTCTTTTACA
TGAGAATAGAGGCTTTTATGCAAAATTGAATGCAGGTTTTTCAGCATATACACAATGTCTT
GTGCAACAGAAAAACATGTTGGGGAAATATTCTCAGTGGAGAGTCGTTCTCATGCTGACGG
GGAGAACGAAAGTGACAGGGGTTTCTCTATAAGTTTTGTATGAAATATCTCTACAAACCTCA
ATTAGTTCTACTCTACACTTTCACTATCATCAACACTGAGACTATCCTGTCTCACCTACAAA
TGTGGAACCTTTACATTGTTTCGATTTTTTCAGCAGACTTTGTTTTATTAAATTTTTATTAGTG
TTAAGAAATGCTAAATTTATGTTTCAATTTTATTTCCAAATTTCTATCTTGTATTATTGTACAA
CAAAGTAATAAGGATGGTTGTACAAAAACAAACTATGCCCTCTCTTTTTTTTCAATCACC
AGTAGTATTTTTGAGAAGACTTGTGAACACTTAAGGAAATGACTATTAAAGTCTTATTTTTTA
TTTTTTTCAAGGAAAGATGGATTCAAATAAATATTTCTGTTTTTGCTTTTAAAAA

FIGURE 112

MWLKVFTTFLSFATGACSGLKVTVPSTVHGVRGQALYLEVHYGFHTPASDIQIIWLFERPH
TMPKYLLGSVNKSVVPDLEYQHKFTMMPPNASLLINPLQFPDEGNYIVKVN IQNGTLSASQ
KIQVTVD DPVTKPVVQIHPPSGAVEYVGNMTLTCHVEGGTRLAYQWLKNGRPVHTSSTYSFS
PQNTLHIAPVTKEDIGNYSLVRNPVSEMESDIIMPIIYYGPGYGLQVNSDKGLKVGEVFTV
DLGEAILFDCSADSHPPNTYSWIRRTDNTTYIIKHGPRLEVASEKVAQKTM DYVCCAYNNIT
GRQDETHFTVIITSVGLEKLAQKGKSLSP LASITGISLFLIISMCLLFLWKYQPYKVIKQK
LEGRPETEYRK AQTFSGHEDALDDFGIYEFVAFPDVSGVSRIPSR SVPASDCVSGQDLHSTV
YEVIQHIP AQQDHP E

Signal sequence:

amino acids 1-18

Transmembrane domain:

amino acids 341-359

N-glycosylation site.

amino acids 73-77, 92-96, 117-121, 153-157, 189-193, 204-208,
276-280, 308-312

Casein kinase II phosphorylation site.

amino acids 129-133, 198-202, 214-218, 388-392, 426-430, 433-437

Tyrosine kinase phosphorylation site.

amino acids 272-280

N-myristoylation site.

amino acids 15-21, 19-25, 118-124, 163-167, 203-209, 231-237,
239-245

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 7-18

FIGURE 113

GCAAGCGGCGAAATGCGGCCCTCCGGGAGTCTTGCACTTCCCTGGCAGTCTTGGTGTCTGT
GCTTTGGGGTGCTCCCTGGAGCGCACGGGCGGCGAGCAACGTTTCGCGTCATCAGCGAGCAGA
ACTGGAGAGAACCTGCTGGAAAGGAGACTGGATGATAGAAATTTATGCCCCGTGGTGCCCTGCT
TGTCAAAATCTTCAACCGGAATGGGAAAAGTTTGTCTGAATGGGGAGAAGATCTTGAGGTTAA
TATTGCGAAAAGTAGATGTCACAGAGCAGCCAGGACTGAGTGGACGGTTTTATCATAACTGCTC
TTCTACTATTTATCATTTGTAAGATGGTGAATTTAGGCGCTATCAGGGTCCAAGGACTAAG
AAGGACTTCATAAACTTTATAAGTGATAAAGAGTGAAGAGTATTGAGCCCGTTTCATCATG
GTTTGGTCCAGGTTCTGTTCTGATGAGTAGTATGTCAGCACTCTTTTCAGCTATCTATGTGGA
TCAGGACGTGCCATAACTACTTTATTGAAGACCTTGGATTGCCAGTGTGGGGATCATATACT
GTTTTTGCTTTAGCAACTCTGTTTTCCGGACTGTTATTAGGACTCTGTATGATATTTGTGGC
AGATTGCCCTTTGTCCTTCAAAAAGGCGCAGACCACGCCATACCCATACCCCTTCAAAAAAT
TATTATCAGAATCTGCACAACCTTTGAAAAAAGTGGAGGAGGAACAAGAGGCGGATGAAGAA
GATGTTTCAGAAGAAGAAGCTGAAAGTAAAGAGGAACAACAAAGACTTTCCACAGAATGC
CATAAGACAACGCTCTCTGGGTCCATCATTTGGCCACAGATAAATCCTAGTTAAATTTTATAG
TTATCTTAATATTATGATTTTGATAAAAAACAGAAGATTGATCATTTTGTTTGGTTTGAAGTG
AACTGTGACTTTTTTGAATATTGCAGGGTTCACTCTAGATTGTCTATTAATTTGAAGAGTCTA
CATTCAGAACATAAAAGCACTAGGTATACAAGTTTGAAATATGATTTAAGCACAGTATGATG
GTTTAAATAGTTCTCTAATTTTTGAAAAATCGTGCCCAAGCAATAAGATTATGTATATTTGT
TTAATAATAAACCTATTTCAGTCTGAGTTTTGAAAAATTACATTTCCCAAGTATTGCATTAT
TGAGGTATTTAAGAAGATTATTTTAGAGAAAAATATTTCTCATTGATATATAATTTTCTCTG
TTTCACTGTGTAAAAAAGAAGATATTTCCCATAAATGGGAAGTTTGCCCATTTGCTCAAG
AAATGTGATTTTCAGTGACAATTTTCGTGGTCTTTTAGAGGTATATTTCCAAAATTTCCCTGT
ATTTTAGGTTATGCACTAATAAAAACTACCTTACATTAATTAATTACAGTTTTCTACACA
TGGTAATACAGGATATGCTACTGATTTAGGAAGTTTTTAAGTTCATGGTATTCTCTTGATTCT
CAACAAAAGTTTGATTTTCTCTGTATTTTCTTACTTACTATGGGTACATTTTTTATTTTT
CAAAATGGATGATAATTTCTTGGAACAATTTTTATGTTTTAGTAAACAGTATTTTTTGT
GTTTCAAACTGAAATTTACTGAGAGATCCATCAAATTGAACAATCTGTTGTAATTTAAAAT
TTGGCCACTTTTTTCAGATTTTACATCATTTCTGTGAACTTCAACTTGAAATTTGTTTTTT
TTTCTTTTGGATGTGAAGGTGAACATTTCTGATTTTTTGTCTGATGTGAAAAAGCCTTGGTA
TTTTACATTTTGAAAAATTCAAAGAAGCTTAATATAAAGTTTGCAATTTACTCAGGAAAAAG
CATCTCTTGATATATGCTTAAATGTATTTTTGTCTCATATACAGAAAGTTCTTAATTGAT
TTTACAGCTGTAATGCTTGATGTTTTAAAATAATAACATTTTTATATTTTTTAAAAGACAA
ACTTCATATTATCCTGTGTTCTTTCTCTGACTGGTAATATTGTGTGGGATTTCCACAGGTAAAA
GTCAGTAGGATGGAACATTTTAGTGATTTTTACTCTTAAAGAGCTAGAATACATAGTTTTT
CACCTTAAAGAAGGGGAAAAATCATAAATACAATGAATCAACTGACCATTCAGTAGTAGAC
AATTTCTGTAATGTCCCTTCTTTCTAGGCTCTGTTGCTGTGTGAATCCATTAGATTTACAG
TATCGTAATATACAAGTTTTCTTTAAAGCCCTCTCTTTAGAATTTAAAATATTGTACCATT
AAAGGTTTGGATGTGTAACCTGTGATGCCCTAGAAAAATATCCTAAGCACAAAATAAACCT
TCTAACCACTTCATTAAAGCTGAAAAAATTTTTTTTTT

FIGURE 114

MAPSGSLAVPLAVLVLLLWGAPWTHGRRSNVRVITDENWRELLEGDWMIEFYAPWCPACQNL
QPEWESFAEWGEDLEVNIKVDVTEQPGLSGRFIITALPTIYHCKDGEFRRYQGPRTKKDFI
NFISDKEWKSIEPVSSWFGPGSVLMSSMSALFQLSMWIRTNCHNYFIEDLGLPVWGSYTVFAL
ATLFSGLLLGLCMIFVADCLCPSKRRRPQYPYPYPSKLLSESAQPLKKVEEQEAEDEEDVSE
EEAESKEGTNKDFPQNAIRQSLGPSLATDKS

Signal sequence:

amino acids 1-26

Transmembrane domain:

amino acids 182-201

Casein kinase II phosphorylation site.

amino acids 68-72, 119-123, 128-132, 247-251, 257-261

Tyrosine kinase phosphorylation site.

amino acids 107-115

N-myristoylation site.

amino acids 20-26, 192-198

Amidation site.

amino acids 25-29

FIGURE 115

GCGAGTGTCCAGCTGCGGAGACCCGTGATAATTCGTTAACTAATTCAACAAACGGGACCCTT
CTGTGTGCCAGAAACGCAAGCAGTTGCTAACCCAGTGGGACAGGCGGATGGAAAGAGCGGG
AAGGTCTTGGCCCCAGAGCAGTGTGACACTTCCTCTGTGACCATGAAACTCTGGGTGTCTGC
ATTGCTGATGGCCTGGTTTGGTGTCTGTGAGCTGTGTGCAGGCCGAATTCTTCACCTGATTG
GGCAGATGACTGACCTGATTATGCAGAGAAAAGAGCTGGTGCAGTCTCTGAAAGAGTACATC
CTTGTGGAGGAAGCCAAGCTTTCCAAGATTAAGAGCTGGGCCAAACAAAATGGAAAGCCTTGAC
TAGCAAGTTCAGCTGCTGATGCTGAGGGGTACCTGGCTCACCTGTGAATGCCTACAAACTGG
TGAAGCGCTAAACACAGACTGGCCTGCGCTGGAGGACCTTGTCTGTGAGGACTCAGCTGCA
GGTTTTATCGCCCAACCTCTCTGTGCAGCGGCAGTTCTTCCCCACTGATGAGGACGAGATAGG
AGCTGCCAAAGCCCTGATGAGACTTCAGGACACATACAGGCTGGACCCAGGCACAATTTCCA
GAGGGGAACCTCCAGGAACCAAGTACCAGGCAATGCTGAGTGTGGATGACTGCTTTGGGATG
GGCCGCTCGGCTACAATGAAGGGGACTATTATCATACGGTGTGTGGATGGAGCAGGTGCT
AAAGCAGCTTGATGCCGGGGAGGAGGCCACCACAACCAAGTACAGGTGCTGGACTACCTCA
GCTATGCTGTCTTCCAGTTGGGTGATCTGCACCGTGCCCTGGAGCTCACCCGCGCCTGCTC
TCCCTTGACCCAAAGCCACGAACGAGCTGGAGGGGAATCTGCGGTACTTTGAGCAGTTATTGGA
GGAAGAGAGAGAAAAACGTTAAACAAATCAGACAGAAGCTGAGCTAGCAACCCAGAAAGGCA
TCTATGAGAGGCGCTGTGGACTACCTGCCTGAGAGGGATGTTTACGAGAGCCTCTGTCTGGG
GAGGTGTCAAACCTGACACCCCTAGACAGAAGAGGCTTTTCTGTAGTACCACCATGGCAA
CAGGGCCCCACAGCTGCTCATTGCCCCCTTCAAAGAGGAGGACGATGGGACAGCCCGCACA
TCGTCAGGTACTACGATGTCTGTCTGATGAGGAAATCGAGAGGATCAAGGAGATCGCAAAA
CCTAAACTTGCACGAGCCACCGTTTCGTGATCCCAAGACAGGAGTCTCTCACTGTCGCCAGCTA
CCGGGTTTCCAAAAGCTCTTGGCTAGAGGAAGATGATGACCCCTGTTGTGGCCCCAGTAAATC
GTCGGATGCAGCATATCACAGGGTTAACAGTAAAGACTGCAGAAATTGTTACAGGTTGCAAA
TATGGAGTGGGAGGACAGTATGAACCGCACTTCGACTTCTCTAGGCGACCTTTTGACAGCGG
CCTCAAAACAGAGGGGAATAGGTTAGCGACGTTTCTTAACTACATGAGTGATGTAGAAGCTG
GTGGTGCCACCGTCTTCCCTGATCTGGGGGCTGCAATTTGGCCTAAGAAGGGTACAGCTGTG
TTCTGGTACAACCTCTTGCAGAGCGGGGAAGGTGACTACCGAACAAGACATGCTGCCTGCC
TGTGCTTGTGGGCTGCAAGTGGGTCTCCAATAAGTGGTTCCATGAACGAGGACAGGAGTTCT
TGAGACCTTGTGGATCAACAGAAGTTGACTGACATCCTTTCTGTCTTCCCTTCTCTGGTC
CTTCAGCCCATGTCAACGTGACAGACACCTTTGTATGTTCTTTGTATGTTTCTATCAGGCT
GATTTTTGGAGAAATGAATGTTTGTCTGGAGCAGAGGGAGACCATACTAGGGCGACTCCTGT
GTGACTGAAGTCCCGCCCTTCCATTAGCCTGTGCCATCCCTGGCCCCAAGGCTAGGATCA
AAGTGGCTGCAGCAGAGTTAGCTGTCTAGCGCTAGCAAGGTGCCTTTGTACCTCAGGTGTT
TTAGGTGTGAGATGTTTCAGTGAACCAAGTTCTGATACCTTGTTTTACATGTTGTTTTAT
GGCATTCTATCTATTGTGGCTTTACCAAAAAATAAAATGTCCCTACCAGAAAAA

FIGURE 116

MKLWVSALLMAWFGVLSCVQAEFFTSIGHMTDLIYAEKELVQSLKEYILVEEAKLSKIKSWA
NKMEALTSKSAADAEGYLAHPVNAYKLVKRLNTDWPALDELVLQDSAAGFIANLSVQRQFFP
TDEDEIGAALKMRLQDTYRLDPGTISRGEPLGTYQAMLSVDDCFGMGRSAYNEGDIYYHTV
LWMEQVLKQLDAGEEATTTKSSQVLDYLSYAVFQLGDLHRALELTRRLSLDPSHERAGGNLR
YFEQLLEEBEREKTLTNQTEAELATPEGIYERFPVDYLPERDVYESLCRGEVVKLTTPRQKRLF
CRYHHGNRAPQLLIAPFKEEWDSPHIVRYYDVMSDEEIERIKKIAKPKLARATVRDPKTG
VLTVASYRVSKSSWLEEDDPVVARVNRMMQHTGLTVKTAELLQVANYGVGGQYEPHFDFS
RRPFDGLKTEGNRLATFLNYMSDVEAGGATVFPDLGAALWPKKGTAVFWYNLLRSGEGDYR
TRHAACPVLVGCKWVSNKWFERHGQEFRLPCGSTEV

Signal sequence:

amino acids 1-17

N-glycosylation site.

amino acids 115-119, 264-268

Glycosaminoglycan attachment site.

amino acids 490-494

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 477-481

Casein kinase II phosphorylation site.

amino acids 43-47, 72-76, 125-129, 151-155, 165-169, 266-270,
346-350, 365-369, 385-389, 457-461, 530-534

Tyrosine kinase phosphorylation site.

amino acids 71-80, 489-496

N-myristoylation site.

amino acids 14-20, 131-137, 171-177, 446-452

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 8-19

Leucine zipper pattern.

amino acids 213-235

FIGURE 117

GCAGTATTGAGTTTACTTCCTCCTCTTTTATGTGGAAGACAGACCATAATCCAGCTGTGAGTGAAATTGATTGT
TTCAATTATTACCGTTTGGCTGGGGGTAGTTCGACACCTTCAACAGTTGAAGAGCAGGCAGAGGAGTTGTGA
AGACAGGACAACTCTTCTGGGGATGCTGGTCTTGGAAGCCAGCGGGCTTGTCTGTCTTTTGGCCTCATGACCC
CAGGTTCTCTGGTTAACTGAAAGCCTACTACTGGCCTGGTGCCATCAATCCATTGATCCTTGAGGCTGTGCC
CTTGGGGCACCCACTTGGCAGGGCTTACCACCATGCGACTGAGCTCCCTTTGGCTCTGCTTGGCGCCAGCGCTTC
CCTCATCTTAGGGCTGTCTCTGGGGTGAGCCTGAGCCTCTCTCGGGTTTCTCGGATCCAGGGGGAGGGAGAAG
ATCCCTGTGTCTGAGGCTGTAGGGGAGCGAGGAGGGCCACAGAATCCAGATTCCAGAGACTCGGCTAGACCAAGTG
ATGAAGACTTCAAAACCCGGATTGTCCCTACTACAGGGACCCCAACAAGCCCTACAAGAAGGTGTCTCAGGACTC
GGTACATCCAGACAGAGCTGGGCTCCCGTGAGCGGTTGTCTGGTGGCTGTCTGACCTCCGAGCTCACTGTGCCA
CTTTGGCCGTGGCTGTAACCGTACGCTGGCCCTCACTTCCCTCGGTACTCTACTTCACTGGGCGAGCGGGGG
CCCGGCTCCAGCAGGATGCAAGTGGTGTCTCATGGGGATGAGCGGCCCGCTGGCTCATGTACAGACCTCTGC
GCCACCTTCAACACACTTTGGGGCGACTACGACTGGTTTTCATCATGAGGATGACATATGTGCGAGCC
CCCGCTGGCAGCCCTTGTCTGGCCACCTCAGCATCAACCAAGACTGTACTTAGGCCGGCAGAGGAGTTCAATG
GGCAGGCGAGCAGGCGCGGTACTGTCTATGGGGCTTTGGCTACCTGTGTTCAGCGAGTCTCTGCTTCTGCTGC
GGCCACATCTGGATGGCTGCGGAGGAGACATTCTCAGTGCCCTTCCCGTGACCCCTGTCTCCGAAGGTACCTCATGT
ACTCTCTGGGCTCGGCTGTGTCTCAACAGCACCAGGGCGAGCAGTATCGCTCACTTTGAACTGGCCAAAAATAGGG
ACCCTGAGAAGGAAGGAGCTCGGCTTCTCAGTGCCCTTCCCGTGACCCCTGTCTCCGAAGGTACCTCATGT
ACCGCTCCAAACACGCTTACGCGCTCTGGAGTTGGAGCGGGCTTACAGTGAAATAGAACAACTGCGAGGCTCAGA
TCCGAACCTTGACCGTGTGACCCCGAAGGGGAGGCGGGCTGAGCTGGCCCGTTGGGCTCCCTGCTCCTTTCA
CACCACACTCTCGCTTTGAGTGTCTGGGCTGGGACTTTCACAGAGCAGCACCTCTCTCTGTGAGATGGGG
TCCCAAGTGGCCACTACAGGGGGCTAGCAGGGCGGACGTGGGTGATGCGTTGGAGACTCGCCTGGAGCAGCTCA
ATCGCGCTATCAAGCCCGCTCGGCTTCAGAAAGCAGCGACTGCTCAACGGCTATCGCGCTTGCAGCCAGCAC
GGGCGATGGATACACCTTGACCTGCTGTTGGAATGTGTGACACAGCGTGGGCACCGCGGGCCCTGGCTCGCA
GGGTGAGCTGTGCGGCCACTGAGCGGGGTGGAATCCTACCTATGCCCTATGTCACTGAGGCCACCGAGTGC
AGCTGGTGTGCTGCCACTCTCGTGGCTGAAGTGTCTGACGCCCGGCTTCTCTCAGGCGCTTGCAGCAATGTCC
TGGAGCCACGAGAACATGCAATTGCTCACCTGTTGTGTGTCTACGGGCCACGAGAAGGTGGCCGTGGAGCTCAG
ACCCATTCTTGGGGTGAAGGTGACAGCAGCGGAGTTAGAGCGACGTAACCTGGGACGAGGCTGGCCTGGCTCG
CTGTGCGAGCAGAGGCCCTTCCAGGTGCGACTCATGGAAGTGGTCTCAAGAAGCACCCCTGTGGACACTCTCT
TCTTCTTACCACCGTGTGGACAAGGCTGGGCCCGAAGTCTCAACCGCTGTGCAATGAATGCCATCTCTGGCT
GGCAGGCTTCTTTCCAGTCCATTCCAGGAGTTCAATCTGCCCTGTCAACACAGAGATACCCCCAGGGCCCC
CGGGGGCTGGCCTGACCCCCCTCCCTCTCTGTGCTGACCCCTCCGGGGGGCTCCTATAGGGGGGAGATTTG
ACCGGAGGCTTCTCGGAGGGCTGCTTCTCAACGCTGACTACTGGCGGCCCGAGCCCGCTGGCAGGTGAAC
TGGCAGGCAGGAAGAGGAGGAAGCCCTGGAGGGGCTGGAGGTGATGGATGTTTCTCCTCGGTTCTCAGGGCTCC
AGCTCTTTTGGGGCGTATAGAGCAGGGCTGGTGCAAGATTCTCCTCGGAGACTCAGGCCACCGCTCAGTGAAG
AACTCTAACCCGCTGCGGCCCTCAGCAACCTGGAAGGGGCTAGGGGGCCGTGCCACGCTGCTTGTGCTCTCT
AGCAGGAGCAGGCCAATAGCACTTAGCCCGCTGGGGCCCTAACCTCATTAACCTTTCTCTTGTCTGCTCAGCC
CCAGGAGGGCAAGGCAAGATGGTGGACAGATAGAGAATTGTTGCTGTATTTTAAATATGAAAATGTTATTAA
ACATGTCTCTGCG

FIGURE 118

MRLSSLLALLRPALPLILGLSLGCSLSLLRVSWIQEGEDPCVEAVGERGGPQNPDSSRARLD
QSDDEFKPRIVPYRDPNPKPYKKVLRTRYIQTELGSRERLLVAVLTSRATLSTLAVAVNRVT
AHFFPRLLYFTGQRGARAPAGMQVVSHGDERPAWLMSETLRHLHTHFGADYDWFIMQDDTY
VQAPRLAALAGHLSINQDLYLGRAEEFIGAGEQARYCHGGFGYLLSRSLLLRLRPHLDGCRG
DILSARPDDEWLGRCLIDSLGVGCVSQHQGQQYRSFELAKNRDPEKEGSSAFLSAFAVHPVSE
GTLMYRLHKRFSALELERAYSEIEQLQAQIRNLTVLTPGEAGLSWPVGLPAPFTPHSRFEV
LGWDYFTEQHTFSCADGAPKCP LQGASRADVGDALETALEQLNRRYQPRLRFQKQRLNGYR
RFDPARGMEYTLDDLLECVTQRGHRRALARRVSLRLPLSRVEILMPYVTEATRVQLVLP LL
VAEAAAAAPAFLEAFAANVLEPREHALLTLLLVYGPREGGRGAPDPFLGVKAAAELERRYPG
TRLAWLAVRAEAPSQVRLMDVVSKKHPVDTLFFLT TVWTRPGPEVLNRCRMNAISGWQAFPP
VHFQEFNPALSPQRSPPGPPGAGDPSPSPGADPSRGAPIGGRFDRQASAEAGCFYNADYLA
RARLAGELAGQEEEEALEGLEVMDFLRFSGHLHFRAVEPGLVQKFSRLDCSPRLSEELYHR
CRLSNLEGLGGRAQLAMALFEQE QANST

Signal sequence:

amino acids 1-15

Transmembrane domain:

amino acids 489-507

N-glycosylation site.

amino acids 121-125, 342-346

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 319-323, 464-468

Casein kinase II phosphorylation site.

amino acids 64-68, 150-154, 322-326, 331-337, 368-372, 385-389,
399-403, 409-413, 473-477, 729-733, 748-752

Tyrosine kinase phosphorylation site.

amino acids 736-743

N-myristoylation site.

amino acids 19-25, 23-29, 136-142, 397-403, 441-447, 544-550,
558-564, 651-657, 657-663, 672-678

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 14-25

Cell attachment sequence.

amino acids 247-250

FIGURE 119

CGGAGTGGTGCGCCAACGTGAGAGGAAACCGTGCGCGGCTGCGCTTTCTGTCCCCAAGCC
GTTCTAGACGCGGGAATAATGCTTTCTGAAAGCAGCTCCTTTTTGAAGGTTGTGATGCTTGG
AAGCATTTTCTGTGCTTTGATCACTATGCTAGGACACATTAGGATTGGTCATGGAAATAGAA
TGCACCACCATGAGCATCATCACCTACAAGCTCCTAACAAAGAAGATATCTTGAAAAATTTCA
GAGGATGAGCGCATGGAGCTCAGTAAGAGCTTTTCGAGTATACTGTATTATCCTTGTAACC
CAAAGATGTGAGTCTTTGGGCTGCAGTAAGGAGACTTGGACCAACACTGTGACAAAGCAG
AGTTCCTTCAGTTCTGAAAAATGTTAAAGTGTTCGAGTCAATTAATATGAGACAAATGACATG
TGGTTAATGATGAGAAAAGCTTACAAATACGCCTTTGATAAGTATAGAGACCAATACAACCTG
GTTCTTCCTTGACGCCCCACTACGTTTGCTATCATTGAAAACCTAAAGTATTTTTTGTAA
AAAAGGATCCATCACAGCCTTTCTATCTAGGCCACACTATAAACTGAGAGCCTTGAATAT
GTGGGTATGGAAGGAGGAATGTCTTAAGTGTAGAATCAATGAAAAGACTTAACAGCCTTCT
CAATATCCCAGAAAAGTGTCTGAACAGGGAGGGATGATTTGGAAGATATCTGAAGATAAAC
AGCTAGCAGTTTGCTGAAATATGCTGGAGTATTTGCAGAAAATGCAGAAGATGCTGATGGA
AAAGATGTATTTAATACCAAATCTGTTGGGCTTTCTATTAAAGAGGCAATGACTTATCACCC
CAACCAGGTAGTAGAAGGCTGTTGTTTCAGATATGGCTGTTACTTTTAATGGACTGACTCCAA
ATCAGATGCATGTGATGATGTATGGGGTATACCGCCTTAGGGCATTGGGCATATTTTCAAT
GATGCATTGGTTTTCTTACCTCCAAATGGTTCTGACAATGACTGAGAAGTGGTAGAAAAGCG
TGAATATGATCTTTGTATAGGACGTGTGTTGTCATTATTTGTAGTAGTAACATACATATCCAA
TACAGCTGATGTTTCTTTTCTTTTCTAATTGGTGGCACTGGTATAACACACATTAAG
TCAGTAGTACATTTTAAATGAGGGTGGTTTTTTCTTTAAACACATGAACATTGTAAATG
TGTGGAAGAAGTGTTTAAGAATAATAATTTGCAAATAAATATTAATAAATATTATAT
GTGATAAATTCTAAATATGAACATTAGAAATCTGTGGGCACATATTTTGCTGATTGGTT
AAAAAATTTTAAAGGTCTTTAGCGTTCTAAGATATGCAAAATGATATCTCTAGTTGTGAATT
TGTGATTAAAGTAAACTTTTAGCTGTGTGTTCCCTTTACTTCTAATACTGATTTATGTTCT
AAGCCTCCCCAAGTTCCAATGGATTGCGCTTCTCAAATGTACAACCTAAGCAACTAAAGAAA
ATTAAAGTGAAAGTTGAAAAAT

FIGURE 120

MLSESSSFLKGVMLGSIFCALITMLGHIRIGHGNRMHHHEHHHLQAPNKEDILKISEDERME
LSKSFRVYCIILVKPKDVSLSWAAVKETWTKHCDKAEFFSSENVKVFESINMDTNDMWLMMRK
AYKYAFDKYRDQYNWFPLARPTTFAI IENLKYFLCLKDPSQPFYLGHTIKSGDLEYVGMGG
IVLSVESMKRLNSLLNIPEKCPEQGGMWKISEDKQLAVCLKYAGVFAENAEDADGKDVFNT
KSVGLSIKEAMTYHPNQVVEGCCSDMAVTFNGLTPNQMHVMMYGVYRLRAFGHIFNDALVFL
PPNGSDND

Signal sequence:

amino acids 1-33

N-glycosylation site.

amino acids 121-125, 342-346

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 319-323, 464-468

Casein kinase II phosphorylation site.

amino acids 64-132, 150-154, 322-326, 331-335, 368-372, 385-389,
399-403, 409-413, 473-477, 729-733, 748-752

Tyrosine kinase phosphorylation site.

amino acids 736-743

N-myristoylation site.

amino acids 19-25, 23-29, 136-142, 397-403, 441-447, 544-550,
558-564, 651-657, 657-663, 672-672

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 14-25

Cell attachment sequence.

amino acids 247-250

Abstract The purpose of this study was to determine the effect of a 12-week training program on the heart rate (HR) and blood pressure (BP) of sedentary, middle-aged men. The subjects were divided into two groups: a control group and an exercise group. The exercise group performed a 12-week training program consisting of three sessions per week, each lasting 30 minutes. The control group did not exercise. The HR and BP were measured at baseline and at the end of the 12-week period. The results showed that the exercise group had a significant decrease in both HR and BP compared to the control group. The HR decreased from 72 to 68 beats per minute, and the BP decreased from 120/80 to 110/70 mmHg. The control group showed no significant change in HR and BP. These findings suggest that a 12-week training program can effectively reduce HR and BP in sedentary, middle-aged men.

[illegible]

FIGURE 122

MNSSKSSETQCTERGCFSSQMFLWTVAGIPILFLSACFITRCVVTFRIFQTCDEKKFQLPEN
FTELSCYNYGSGSVKNCCPLNWEYFQSSCYFFSTDITISWALS LKNCSAMGAHLVVINSQEEQ
EFLSYKKPKMREFFIGLS DQVVEGQWQWDGTPLTKSLSFWDVGE PNNIATLEDCATMRDSS
NPRQNWNDVTCFLNYFRICEMVGINPLNKGKSL

Signal sequence:

amino acids 1-42

N-glycosylation site.

amino acids 2-6, 62-66, 107-111

Casein kinase II phosphorylation site.

amino acids 51-55, 120-124, 163-167, 175-179, 181-185

N-myristoylation site.

amino acids 15-21, 74-80, 155-161

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 27-38

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CGAGTACCAAGCCGCGCGCGCTCGCTCGCTGGCCCTCTGCAACACCTCGACATGCGGCTGATGGCGCGACCCGCGAG
TCGGCTCTTCGGCTTCGGCTCGCTGACTGCTTCTCTGCTGCTTTTTCAGGGCTGCGCTGATAGGGGCTGTAAATC
TCAAACTCCAGCAATCGAAACCCAGTGTACAGGAATTTGAAAGTTGTGGAATCTGCTTTGATCAGATCCGATTCGC
AGCAACAGTGACCCCAAGCTCGAGTGGAGAGAAATTCAGAGTGAACAAACCATATGTGTTTTTGACACAATA
TTCAGGAGACTTCGGCGGGTCTGTGCAAAATCTGGGAGAGACATCCCTGGAAGATCTGGAATGTGACACAGAGAT
ACTCAGCCCTTTATTCGCTGTAGGCTGTGTCTCGAAATGAGCCAGCAAGAAATGTGATGAGATTTGATCGAGAGAT
CTGTCCAAGTGAAGCAGACCCCTGTGTGTAGAGTCGGAAGGCTGTACCAGTAGGCGAAGTGGCAACACTGC
ACTGCGACGAGAGATGGAGGCGACACCCCGGCTCCTACACAGCTTGATCTGCAATGATGTACCACTGCCACGGAT
CCAGAGCGAATCCCAAGATTTGCAATTTCTCTTTCTTCTTCCATTAAGTCTGAACAGGCACTTTGGTGTCTACGCT
TTCACAAGGACGACTCTGGGCGACTACTCATGTGTTCTCAATGACGCGAGCTCAGCAGAGTGTGGAGACAGG
AGATGGAAGTCTATGACTGTGAACATTTGGCGAATTTATGGGGGAGTCTTGGTGTCTCTTCTGTACTGGCCCTGA
TCACTGTGGGCACTCTCTGTGATACACAGACGTGGCTACTTCATCAACAATAAACAGATGGGAGAAATGTACAAGA
ACCAGGAGAAACAGATGAGGTAAATCACTGCTCGCATCGCAGTACGAGGAGGGGCACTTCAGACAAGTCACTGTGTTG
TGATCTGAGACCCCGCGCTGTGGCTGGAGAGCGACAGAGCGCAGCTGCACTATCCTGTCTGAAACCTCTGTGCAA
GGCAGCGAGAGCTGATGCTACGACAGAGCTAGACACTCATGCAAGCTTTTTCGTTGTGGCCAAAGTTGACCA
CTACTCTTTCTTACTTAAACAGGACCATGATAGAGAATTTTCTCAAGATGGCCCGGTAAATATAACCAACA
GGAAGCGAAATGGGTGGCTCATGTAGTTGGGTTCTTAATCTGTTTGTGGCGTATTCCGCGATGAGTATTAGG
GTGATCTTAAAGAGTTTGTCTGACTAARCCGCCGCTGTGGCCCTGTGGAAGCGCAGATCTTCCACCTGTGCTGT
CAGCGCACGACAGACAGCATGTAGATGGGAGGTGCGTGGACAGCAGCAGAGCGCATCCCGCGGGAAACCA
GAAAGAGGATCTTACACAGAGGCTTACTTCTATCGGCCACAGACACACCGAGATTTCTTCTTAAAGGCTCTGC
TGATCGGTTGTGCACTGTCCATTTGTGGAGAAGCTTTTGGATGACGATTTTGTATTTAAACAAACCAAAATCAGGAAG
GTAAATTCGTTGTGCGAAGAGGATCTTGGCTAGGAGACCTGTGTTCCACAGGCTGTTCAGGATTTTAAGGAA
ACCTATGCTTTAGCTTAAGTCTGAATGTGCTATGAAATGCTTTTCTATGGGCTTGTGTTATTTTATAAAATTT
TACATCTAAATTTTTCGTAAGGATTTTGTGATTTGATTAAGAAGAAATTTCTATTTAAAGCTTAAGATTAATGTT
TACATAAGTTTAAATAACTATTTTTTAAAGAGTTCAACTAAGGTAGAAGTTCCAGAGCTACTAGTGTGTTAAAT
TGGAAATATCAATAATTAAGAGTATTTGAAACAGSAACTCTCTATGGAAGTTACTGTGATGTCTCTTTCT
CACACAGTTTTCGCTTTTTCACAAAGGAACTCACTGTCTACATCAGACATAGTTGCTTGAAGAACTT
TAAAAATTCAGTTTAAGCATGTGAAATCAGTTTGCACTCTTCAAAAGAACTCTCAGGTTAGCTTTGAACT
GCCTCTCTCTGATGATGATGACAGGCTGTGACCCAGAGGCCACCCAGAGCTCAGATGTACATACAGATG
CCAGTCAGCTCTCGGGTGTGGCGCAGGCGCCCGGCTCAGTCTACATGTTGGCTCGCTGTCCGACAGAGCCCT
GCATCTCTGGGCGCTGGCAGTGCGCTGTGTTCCAGTGAAGCTTATCTACAGTGGCCCTTGTCTATCCAGCAGC
TTCAGGTGCGACA CTG CAGGAGACATGTGTTGTCTTCAGTGTGCTCCGACCTTTGGGCTCCTGTAA CAGACCTCT
TTTGGTGTATGATGGCTCTCAAAATAGGCGCCCCAAGTGTATTTTTTTTTTAGGTTTGTGTTTAAATTTGT
AGATTTGTATAGGCGCAAGGCACTGTGCAAAATCAGTCTGTGCAAGTACAATAACAATTTTAAAGAAATTTGAT
CCGACTGTTCTCTTTTGGCAGAGAAAGACA CCGACGCGCACAGGCTCTGTCTGCAATTTCAAAACAAACATGAT
GGATGGGCGGCGCACTCGAGCTCTTTAAAGACCTCAGGTGGAGCAGCAGGTTGAAGGCTCGCGGGGAGGAAGT
TGAAGCCGCTGAAATCAAAAGCACTTTCTTAATTTGACTTTAAATTTTCATCTCGCGGAGACACTGCTCCCAT
TGTGGGGGAGCAATTAGCAACATCACTCAGAAGCTGTGTTCTCAAGAGCAGGTGTTCTCAGCCTCAGTGCCTCT
CGCTGCTGGACTCAGGACTGAAGTGTGTTTAAAGCAGGAGCTGCTGAGGAGGACATCCACTGTGTGCTCGGA
GAATGCTCTCACTACTCACTGTCTTCACTCAGCTTCAAGTGTCTTGGGTTTTATATCTTACAGCTTTTTTTT
AATGTGATACATGAGACTGTGTTGACTTTTGTAGTTGTGAAACACTTGGCGAGCGCCCTGGCAGAGGCA
GGAATGCTCTCAGCAGTGGCTCAGTGTCCCTGGTGTCTGCTCATGCACTCTCGATGCTCTAGCATGCAAGTCT
CCTCTCATATTGCTCAGCTTGTGGAGAGGAGTGGTCTCCCACTCAGCGTTGGGAGTACAGCTCTCAGCTCTCT
TCTTGGTTGTCTATGATGATAGGTAGCTCTTGTGCCCTCTCTTATACCTTAAACAACTCTACACTAGTGGCA
TGGAAACGAGGTCTGAAAGATGATGAGAGAGTGAAGTAGAGTCTGGGAGTAGTCTGCTATAGCTGAGACATGA
CGGAAAGGAAGTCTGCTGATTTTAAAGATGAATGTGACTCAAGACTCAGGCGGACATGAGGCTGTGATTCT
GCCTTTGGATGGATGTGCTGTACACAGAGCTACAGACTGTGACTAACACACCGTAATTTGGCATTTGTTTAACT
CTCATTTATAAAGCTCTCAAAAACACCA

FIGURE 124

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA77624

><subunit 1 of 1, 310 aa, 1 stop

><MW: 35020, pI: 7.90, NX(S/T): 3

MALRRPPRLRLCARLPDFFLILLFRGLIGAVNLKSSNRTPVQEFESVELSCIITDSQTS
PRIEWKKIQDEQTTYVFFDNKIQGDLAGRAEILGKTSLSKIWNVTNRDSALYRCEVVARNDRK
EIDEIVIELTVQVKPVTVCVRPKAVPVGKMATLHCQSESGHPRPHYSWYRNDVPLPTDSRA
NPRFRNSSFFHLNSETGTLVFTAVHKDDSGQYYCIASNDAGSARCEEQEMEYVDLNIGGIIGG
VLVVLAVLALITLGICCAYYRRGYFINNKQDGESYKNPGKPDGVNYIRTDEEGDFRHKSSFVI

Important features of the protein:

Signal peptide:

amino acids 1-30

Transmembrane domain:

amino acids 243-263

N-glycosylation sites.

amino acids 104-107, 192-195

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 107-110

Casein kinase II phosphorylation site.

amino acids 106-109, 296-299

Tyrosine kinase phosphorylation site.

amino acids 69-77

N-myristoylation sites.

amino acids 26-31, 215-220, 226-231, 243-248, 244-249, 262-267